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OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 20:19:38 ; Search time 50.07 Seconds

(Without alignments)
4863.166 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGAGCCCTGTGACT.....GCTTCACATTAGAGCCG 1610

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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7: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
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1	1610	100.0	1610	5	US-08-889-108-7
2	1610	100.0	1610	6	PCT-US94-10358-7
3	1123.8	69.8	1618	5	US-08-889-108-1
4	1123.8	69.8	1618	5	US-08-889-108-3
5	1123.8	69.8	1618	6	PCT-US94-10358-1
6	1123.8	69.8	1618	6	PCT-US94-10358-3
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8	443.2	27.5	2272	5	US-08-147-592A-3
9	416.4	25.9	1410	5	US-08-147-592A-1
10	385.6	24.0	1000	5	US-08-147-592A-11
11	363.8	22.6	1567	5	US-08-889-108-16
12	363.8	22.6	1567	6	PCT-US94-10358-16
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39	102.6	6.4	678	1	US-07-915-966C-3	Sequence 3, Appl
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41	102.6	6.4	678	5	US-08-853-194-3	Sequence 3, Appl
42	102.2	6.3	563	1	US-07-915-966C-2	Sequence 2, Appl
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44	102.2	6.3	563	5	US-08-853-194-2	Sequence 2, Appl
45	97.2	6.0	1586	2	US-08-461-244-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-889-108-7
Sequence 7, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-889-108-7
Query Match 100.0%; Score 1610; DB 5; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
PCT-US94-10358-7
Sequence 7, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT: MW OPIOID RECEPTORS: COMPOSITIONS AND METHODS
TITLE OF INVENTION: 17
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
type: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 PCT-US94-10358-7

Query Match 100.0%; Score 1610; DB 6; Length 1610;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
 US-08-889-108-1
 : Sequence 1, Application US/08889108
 : Patent No. 6103492
 : GENERAL INFORMATION:
 : APPLICANT: Yu, Lei
 : TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee
 : STREET: P. O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/889,108
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/305,518
 : FILING DATE:

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3

Query Match 69.8%; Score 1123.8; DB 5; Length 1618;
Best Local Similarity 83.7%; Pred. No. 7.9e-291;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

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2 GTGGAAGGGGGCTACAGAGAGAGAAATACAGACGCTCAGA-CGTTCCTCTTGCTG 60
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61 CCCTCTCTCTGTTCTACATAGAGGCTGCTCATGTAAGATCTGACGAGACCTAGGGCA 120
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1435 TCGCTAAGCTTAAAGCCACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1494
1526 GCTCTAATCTTAAAGCCACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1585
1495 GCTCTGATTTTCTGAGAGAA---CATCTGATCTGCTGATTCAAAGTATCTCTTGCT 1551
1586 ACTCTGCTGACATTTAG 1606
1552 ACTTCACTCTGACATGAGAG 1572

RESULT 5
PCT-US94-10358-1
Sequence 1, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
PCT-US94-10358-1

Query Match 69.8%; Score 1123.8; DB 6; Length 1618;
Best Local Similarity 83.7%; Pred. No. 7.9e-291;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

QY 27 GTGGGAGGGGCTATACGCGAGAGAGATGTCAAGTCTAGCTCCGCTCCGCTG 86
DB 2 GTGGAGGGGGCTACAGAGAGAGATATCAAGCGCTAGA-CGTTCCCTTCTGCTG 60
QY 87 AGCTCTCTCTCTCTCAGCGAGACGCTGTTCTGTAGAGAAACAGCAGAGAG-CTGTGCA 145
DB 61 CGCGCTTCTCTGTTCTCAGCTAGGGCTGTCTCATGTAGATGTGACGAGGCTAGGCA 120
QY 146 GCGGCGAAAGAGAGCGCTGAGCGCTTGGAAACCGAAAGTCTGGTCTGCTGCTAC 205
DB 121 GGTGTAGAGAGAGAGGCTGGGCGGTGGAGACCCGAAAGTCTGAGTCTCAGTTAC 180
QY 206 CTGCGACAGCGTCCCGCGCGCGCTGACGTACATGACGACGCGTGCCTCCACGAAAC 255
DB 181 AGCTCTCTCTCTCTCAGCGAGCGCTTTCAGCACATGACGACGACCGCGCCAGGAAAC 240
QY 266 GCCAGCAATTCAGCTAGCTTGGGCTACTCAAGTTGCTCCGACAGACCCAGCCCGGT 325
DB 241 ACCAGGACTGTCAACCCCTTAGCTCAGGCAAGTGTCTCCCAAGCA-----CTGGGC 294
QY 326 TCTGTGCTCAACTTGTCCCACTTAGATGCGCAACCTGTCCGACCATGCGGTCCGAACCGC 385

DB 295 TCTGTGCTCAACTTGTCCCACTTAGATGCGCAACCTGTCCGACCATGCGGTCCGAACCGC 354
QY 386 ACCGACTGTGGGGGAGAGACACAGCTGTGCTCCGACCGGAGTCCCTCATGATCAG 445
DB 355 ACCGGCTTGTGGGGAGAGACACAGCTGTGCTCCGACCGGAGTCCCTCATGATCAG 414
QY 446 GCCATCAGCAATTCAGCTAGCTTGGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 505
DB 415 GCCATCAGCAATTCAGCTAGCTTGGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 474
QY 506 CTGTGATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 565
DB 475 CTGTGATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 534
QY 566 TTCAACCTTGTCTGTGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 625
DB 535 TTCAACCTTGTCTGTGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 594
QY 626 TACCTATGAGGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 685
DB 595 TACCTATGAGGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 654
QY 686 TACTATATATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 745
DB 655 TACTATATATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 714
QY 746 GCAGTGTGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 805
DB 715 GCTGTGTGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 774
QY 806 AATGTGTGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 865
DB 775 AATGTGTGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 834
QY 866 ACAAAATACAGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 925
DB 835 ACAAAATACAGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 894
QY 926 TGGGAAACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 985
DB 895 TGGGAAACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 954
QY 986 ATTACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1045
DB 955 ATTACGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
QY 1046 TCCAAAGAAAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1105
DB 1015 TCCAAAGAAAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1074
QY 1106 GTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1165
DB 1075 GTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134
QY 1166 ATCCAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1225
DB 1135 ATCCAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
QY 1226 AACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1285
DB 1195 AACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1254
QY 1286 AGAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1345
DB 1255 AGAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
QY 1346 CAGAACTATGAGAGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1405
DB 1315 CAGAACTATGAGAGACACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1374
QY 1406 GAAATCTGGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1465

Db 1375 GAAATCTGAGAGGAGAACTGCTCATTTGCCCTAACTGGGCTCAGACATCCAGACC 1434
QY 1466 TCACCAAGCTTAGAAGCCACCATGTATGTGAGAGAGTTCCTTCACAAATGTAGAGAG 1525
Db 1435 TCAGTAAGCTTAGAGGCGCGCATCTACGTGAGATCAGGTCTGTGACAGGTGTGGGAG 1494
QY 1526 GCTTAATCTCTAGAAAGTGCCTTTTAAAGTCACTCAACCTTCTCTCTGCGC 1585
Db 1495 GCTGTGTTCTCTGAGAAA---CCATCTGATCTGTCATTCAAAAGTCACTTCTCTGCT 1551
QY 1586 ACTCTGCTCTGACATTTAGAG 1606
Db 1552 ACTTCACTCTGACATAGAG 1572

RESULT 6
PCT-US94-10358-3
: Sequence 3, Application PC/TUS9410358
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10358
: FILING DATE: Concurrently herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/120,601
: FILING DATE: 13 SEPTEMBER 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WILSON, MARK B.
: REGISTRATION NUMBER: 37,259
: REFERENCE/DOCKET NUMBER: INDA005P--
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1618 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 339..1235
: PCT-US94-10358-3

Query Match 69.8%; Score 1123.8; DB 6; Length 1618;
Best Local Similarity 83.7%; Pred. No. 7.9e-291;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

QY 27 GTGGAGAGGGGCTATACGAGAGAGATGTCAGATGCTCAGTCCGCTCCGCTG 86
Db 2 GTGGAGAGGGGCTCAAGAGAGAGAGATATACAGCGCTCAGA-CGTTCCCTTTCGCTG 60
QY 87 ACAGCTCTCTCTGTCAGCCAGAGACTGTTCTGTAAAGAAACAGCAGAG-CGTGGCA 145
Db 61 CCGCTCTCTCTGTCAGCCAGAGACTGTTCTGTAAAGAAATCTGACGAGACCTTAGGCA 120

QY 146 GCGGCGAAAGAGAGCGGCTGAGGGCTTGGAAACCCGAAAGTCTCGGTGCTCTGCTAC 205
Db 121 GCTGTAGAGAGAGAGAGCGGCTGGGGCGGTGGAAACCCGAAAGTCTGAGTCTAGTTAC 100
QY 206 CTCGACAGAGCGTGGCGCGCGCGCGGTGAGTACATGAGACAGACAGCGTGGCCCCAGCAAC 253
Db 181 AGCCTACCTAGTCCGACAGAGCGCTTCAAGACCATGAGACAGACAGCGCGCCAGGAGAC 247
QY 266 GCCAGCAATTGCACTGATGCCCTTGGCGTACTCAAGTTGCTCCAGCAGACCCAGCCCGGT 325
Db 241 ACCAGCGACGCTGCTCAGAACCCCTTAGCTCAGGCAAGTGTCTCCAGCA-----CTGGGC 294
QY 326 TCTGCGGTCAACTGTTCCCACTTAGATGAGCAGACCTGTCCAGCCATCGGTCCAGCCG 385
Db 295 TCTGCGGTCAACTGTTCCCACTTAGATGAGCAGACCTGTCCAGCCATCGGTCCAGCCG 354
QY 386 ACCGACCTGGGCGGAGAGAGAGCGCTGGCGCTCCGACCGGACGCTCCCTCATGATCAG 445
Db 355 ACCGCGCTGGCGGAGAGAGAGCGCTGGCGCTCCGACCGGACGCTCCCTCATGATCAG 414
QY 446 GCCATCAGATCATGGCCCTCTACTCATGCTGTGCGTGGGCTCTTGGAACTTC 505
Db 415 GCCATTCACATCATGGCCCTCTACTCATGCTGTGAGTGGGCTCTTGGAACTTC 474
QY 506 CTGGTCATGATGATGATTTGTCAGATACCAACAGATGAAGAGCTCCACCAATCTACAT 565
Db 475 CTGGTCATGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 534
QY 566 TTCAACCTGCTGCTGGGAGATGCTTGGACAGCGTACCGCTCCGCTTCAGAGTGTAT 625
Db 535 TTCAACCTGCTGCTGGGAGATGCTTGGACAGCGTACCGCTTCAGAGTGTAT 594
QY 626 TACCTAATGGAGACATGCGCATTTGGAACATCTTGGCAAGATGATCTCCATAGAT 685
Db 595 TACCTAATGGAGACATGCGCATTTGGAACATCTTGGCAAGATGATCTCCATAGAT 654
QY 686 TACTATAACATGTTCCACAGATATTTACCCCTCGACACCATGATGATGATGATGAT 745
Db 655 TACTATAACATGTTCCACAGATATTTACCCCTCGACACCATGATGATGATGATGAT 714
QY 746 GCAGCTGACACCGCTGCAAGAGCTTATGATTTCCGCTGCTCCGCAATGCAAAATATC 805
Db 715 GCTGTGCGCACCGACGCAAGAGCTTATGATTTCCGCTGCTCCGCAATGCAAAATATC 774
QY 806 AATGCTGCAACTGATGATCTCTCTTCAAGCATGCTCTCTCTGATGATGATGATGAT 865
Db 775 AATGCTGCAACTGATGATCTCTCTTCAAGCATGCTCTCTCTGATGATGATGATGAT 834
QY 866 ACAAAATACAGGAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 925
Db 835 ACAAAATACAGGAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 926 TGGGAAACCTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 985
Db 895 TGGGAAACCTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
QY 986 ATTACGCTGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1045
Db 955 ATTACGCTGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
QY 1046 TCCAAAAGAAAGAGAGAGATCTTCAAGAGATCACAGAGATGATGATGATGATGATGAT 1105
Db 1015 TCCAAAAGAAAGAGAGAGATCTTCAAGAGATCACAGAGATGATGATGATGATGATGAT 1074
QY 1106 GTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1165
Db 1075 GTGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
QY 1166 ATCCGAAATCTAGCTTCAGAGCTTTCTTGGCACTTTCATATGCTAGTTACCA 1225
Db 1135 ATCCGAAATCTAGCTTCAGAGCTTTCTTGGCACTTTCATATGCTAGTTACCA 1194

Oy	1226	AACGCTGCCCTCAACCAGCTCTTTATGCTTTCTGTGAAACCTCCAAAGATGCTTC	1285
Db	1195	AACAGCTGCTGAAATCCAGTTCTTTTACGCTTCCTGTGATGAATACTTCAGAGATGCTTC	1284
Oy	1286	AGAGAGTTCTGTATCCCAACCTCTTCCAACTTGGACCAAAACCTCCACTGGAATTCGT	1345
Db	1255	AGAGAGTTCTGTACCTCCCAACCTCGTCTCAGATGGAACAAACCTCCACTGGAATTCGT	1314
Oy	1346	CAGAACCTAGAACCAACCCCTCCAGGGCCAAATACAGTGGATAGAACTATATCATACGTA	1405
Db	1315	CAGAACCTAGGGAAACATCCCTCCAGGGCTAAATACAGTGGATCGAACTAACCCACGCTA	1374
Oy	1406	GAATATCTGGAGACAGAAATCGTCGCCGTGCCCTAACAGGGTCTCATGCGATTCGCCACT	1465
Db	1375	GAATATCTGGAGGACAGAAATCGTCTCCATTTGCCCTTAACGTGGTCTCACACATCCAGACCC	1434
Oy	1466	TCACCAAGCTTGAAGCCACACATGATGTGGAGACAGGTGGTTCAGAGATGTGGAGAG	1535
Db	1435	TCGTAAGCTTAGAGGCGCCGACATCTACGTGAAATCAGTTGGCTGTCAGAGGGTGTGGAGAG	1494
Oy	1526	GCTTAATTTCTTAGAGAAATGCTGCTTTTATGATATCCAAACCTCTTTCCCTCTGGCC	1585
Db	1495	GCTCTGGTTTCCTGAGAAA---CCATCTGATCTCGATTCAAAGATCATTCCTCTGCTGCT	1551
Oy	1586	ACTCTGCTGCACATATAGAG	1606
Db	1552	ACTTCACTCTGCACATATAGAG	1572

RESULT 7
 US-08-411-859-1
 Sequence 1 / Application US/08411859
 Patent No. 5985600
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 APPLICANT: KEITH JR., DONALD E.
 APPLICANT: EDWARDS, ROBERT H.
 TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
 TITLE OF INVENTION: PHARMACEUTICALS
 TITLE OF INVENTION: PHARMACEUTICALS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,859
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/929,200
 FILING DATE: 13-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: LITHGOW, TIMOTHY J.
 REGISTRATION NUMBER: 36,856
 REFERENCE/DOCKET NUMBER: 22000-20526.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEO ID NO.: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1829 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE

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; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..1144
;
US-08-411-859-1

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Query Match	27.5%	Score 443.2;	DB 4;	Length 1829;
Best Local Similarity	67.3%	Pred. No. 4.1e-109;		
Matches 641; Conservative	0;	Mismatches 308;	Indels 3;	Gaps 1;

QY	432	CCTCATGATCAGGGCCATACATCATATGGCCCTCTACCTCATCTGTGGCGTGGGGC	491
Db	159	CGTCCCTCGGCCCTAGCCATGCGCATATACCGGCGCTCTACTCGGCTGTGTGCGAGTGGGGC	218
QY	492	TCCTTGGAAACTTCCTGGTCATGATGTATGTATGTCAGATATACCAAGATGAACTGCCA	551
Db	219	TTCTGGGCAACTCTCTGCTATGTATTGGCATCGTCCGGTACCAAAATTTGAAGACCCGCA	278
QY	552	CCAAATCTCATATTTTCACACCTTGTCTGGCAGATGGCCCTTACCACACAGTACCCCGGCT	611
Db	279	CCAAATCTCATCTCTTCACATCTGGCTTTGGCTGTATGGCTGGCGCACACAGACGCTGCCCT	338
QY	612	TCCAGATGTGAATTAACCTATATGGGAAACATGGCCATTTTGAACCAATCCCTTTGCAAGATG	671
Db	339	TCCAGACGCCCAAGTACTTGATGTGAAACGTGGCCGCTTTGGCAGAGTGGCTGTGSCAAGCTG	398
QY	672	TGATCTCCATAGATTAATTAATACATGTTCACACGATATTCACCCCTTGCCACCATGAGTG	731
Db	399	TGCTCTCATATGTACTACTACACATATTTCACTAGCATCTTCCACCCCTCACATGATGAGCG	458
QY	732	TTGATGATATCATTTGAGTGTGGCACCCGTGCAAGCCCTTAATTTCCGTAATCCCTCGGA	791
Db	459	TGGACCCCTACATTTGCTGTCTGTGTCACATCCTGTCAABCCCTGGACCTTCCGGACACGACA	518
QY	792	ATGCAAAATTAATCAATGTCTGCACTGGATCCTCTCTTCAAGCCATGTGCTTCTGTAA	851
Db	519	AGGCCAAGCTGATCAATATATGTGATCTGGGATCTTGACTTCAGAGTGTGGGGTCCCATCA	578
QY	852	TGTTCAATGGCTACACACAAAATACAGGCAGGTTCATAGATTGTACTACTACTATCTCTC	911
Db	579	TGGTCAAGGAGTAGACCCAAACCCCGGGAGTGGAGCTGTAATGACATGTCTCAAGTTCCTCCA	638
QY	912	ATCCAACTGTGTAAGTGGGAAACCTCTGAAGATCGTATTTCATCTTCCGCTCATTA	971
Db	639	GTCCCACTGTGTAAGTGGGAAACCTCTGAAGATCGTATTTCATCTTCCGCTCATTA	698
QY	972	TGCCAGTGTATCATTAATACCGTGTCTATGAGATGATGATCTTGGCGCTCAAGAGTGTCC	1031
Db	699	TGCCAGTGTATCATTAATACCGTGTCTATGAGATGATGATGATCTTGGCGCTCAAGAGTGTCC	758
QY	1032	GCATGCTCTCTGGCTCCAAAGAAAGAGACAGATCTTCGAGAGTATACACAGATGGTGC	1091
Db	759	GTCTGCTCTCTGGCTCCAAAGAAAGAGACAGCTCTGGCGCATACACAGAGTGGTGC	818
QY	1092	TGTGTGTGTGGGCTGTGTTTCATCTGCTGTGCACTCCATTCACATTTACGTCATCATTA	1151
Db	819	TGTGTGTGTGGGCTGTGTTTCATCTGCTGTGCACTCCATTCACATTTACGTCATCTG	878
QY	1152	AAGCCTTGGTTACAATC--CCAGAAACTAGCTTCCACAGCTGTTCTTGGCATCTTGCA	1208
Db	879	GGAAGCTGTGTGACATCAATCGCGCGACCACTTGTGTGGCCGCTACATGACATCTGTCA	938
QY	1209	TTGCTGTAAGTTACAAACAAAGTGTGCTCAACACAGTCTTTATGCAATTTGGATGAAA	1268
Db	939	TTGCTGTAAGTTACAAACAAAGTGTGCTCAACACAGTCTTTATGCAATTTGGATGAAA	998
QY	1269	ACTTCAACATGCTCTCAGAGATTTCTGTATCCCAACCTCTTCCAAATATGAGCAACAA	1328
Db	999	ACTTCAACATGCTCTTCCGCAAGCTCTGTGTGCAAGCGCTTGGCGCGCAAGAACCGGCA	1058
QY	1329	ACTTCACTGTAATCGTACAGACACTAGAGACCAACCCCTTCCAGCGCCCATATAC	1380

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 186..1325
US-08-147-592A-1

Query Match 25.9% Score 416.4; DB 5; Length 1410;
Best Local Similarity 65.1% Pred. No. 5.3e-102;
Matches 634; Conservative 0; Mismatches 331; Indels 9; Gaps 1;

QY 433 CTCGATGATCAGGCGCATCATCATGCGCCCTCTACTCTCATCTGCTGCTGGGCGCT 492
DB 347 CTCCTCGGCGCATCCCTGATCATCATCCGCTGCTACTCTGTGTATTTGTGTGGGCTT 406
QY 493 CTTGGAACTCTCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
DB 407 AGTGGGCAATCTCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 466
QY 553 CAACATCTACATTTTCAACCTTGCTCTGGCAGATGCTTACGACCACTGACCTGCTT 612
DB 467 CAACATCTACATTTTCAACCTTGCTCTGGCAGATGCTTACGACCACTGACCTGCTT 526
QY 613 CCAGAGTGTGATTTACCTATGAGGAACATGGCCATTGGACCACTGCTTACCAATAT 672
DB 527 TCAGAGTGTGCTCTACTTATGATTTCTTGCCCTTTGGAGATGTGCTATGGAAGATGT 586
QY 673 GATTCATGATGATTTACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
DB 587 CATTTTCATGCTACTACTACATGATTTTACACATATTTACCTTACCATGATGATGT 646
QY 733 TGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 792
DB 647 GGACGCGTCTATGCTGTGCTGACCCCTGGAAGCTTTGGACCTTGGAAACCTTTGAA 706
QY 793 TGCCAAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852
DB 707 AGCAAGATCATCATCATCTGATTTGCTCTGATCATCTGTTGATATCATGACGAT 766
QY 853 GTTCATGCTACAAATAATACAGGAGTTCATAGATTTGATACCTAACTT----- 906
DB 767 AGTCTTGAGGCGACCAAGTCAAGGAGATGATGATGATGATGATGATGATGATGATGAT 826
QY 907 ---CTCTCATCCACCTGTGCTACTGGGAAACCTGTGGAAGATCTGTGTTTCATCTTCCG 963

DB 827 TCCCTGATGATGATTTCTCTGCTGGGATCTCTTCAATGAAATCTGTCTGCTTTGCG 886
QY 964 CTTCAATATGCGAGTGTCTCATCATACCGTGTGCTATGAGATGATGATGATGATGATGAT 1023
DB 887 CTTTGTGATCCAGTCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 946
QY 1024 GAGTGTGCGCATGCTCTCTGCTGCTCCAAAGAAAGGACAGAAATCTTGCAGAGATCAGCAG 1083
DB 947 GAGTGTGCGGCTCTCTGCTGCTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006
QY 1084 GATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1143
DB 1007 GCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1066
QY 1144 CATCATTAAGCTTGTGCTTACATCCCAAGAACTACATGCTTGTGCTGTGCTTGTGCTGCT 1203
DB 1067 CCGTGTGAGGCTCTGTGAG 1126
QY 1204 CCGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1263
DB 1127 CTGTATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1186
QY 1264 TGAAGACTTCAAGCATGCTCTGAGAGATGCTGTATCCCAACTCTTATGATTTGACCA 1323
DB 1187 TGAAGACTTCAAGCGGTGCTTTAGGAGCTTGTGCTTCCCTATTAAGATGCGATGAGCG 1246
QY 1324 ACAAACTCCACTGCAATTTGCTGACAGACATGAGACCACTCCCTCCAGGCCATATGAT 1383
DB 1247 CCAGAGCAACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1306
QY 1384 GAT 1306
DB 1307 AGGAT 1320

RESULT 10
US-08-147-592A-11
Sequence 11, Application US/08147592A
Patent No. 6096513
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
TITLE OF INVENTION: Opioid Receptor Genes,
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 72210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259

Db 918 GGGAGAGAGACCGAAACCTGCGGGGATATCATCGACTGCTGTGTAGTGTGGCTGTGT 977
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Db 1158 AGTCTGCTGCTGCTTATCCCTGACCGGAGATGAGGATTTCTGATGCTGTGCG 1212

RESULT 13

US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,549
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2706 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
; US-08-454-549-1

Query Match 22.6%; Score 363.8; DB 3; Length 2706;
Best Local Similarity 62.9%; Pred. No. 7.7e-88;
Matches 563; Conservative 0; Mismatches 332; Indels 0; Gaps 0;
QY 450 TCACGATCATGCCCTCTACTCATCTGTGCTGTGGGCTCTTGGAACTTCCTGG 509
Db 252 TCACGATCGTGGGCTCTACTTGTGCTGTGATCGGGGGCTCTGCGGAACCTGCTCG 311

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RESULT 14

US-08-454-552-1
; Sequence 1, Application US/08454552
; Patent No. 6005072
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,552
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Rat brain
TISSUE TYPE: Rat brain
US-08-454-552-1

Query Match 22.6%; Score 363.8; DB 5; Length 2706;
Best Local Similarity 62.9%; Pred. No. 7.7e-88;

Matches 553; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

450 TCACGATCATGCGCTTCTACTCCATCGTGTGCGTGGGCTCTTCGAACTCTCTGG 509
252 TCACCATCGTGGGCTCTACTTGGCTGTGATCGGGGGCTCTCGGGAAGTGGCTCG 311
510 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
312 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
570 ACCTTGCTGGGAGATGCTTGAACCATGCTTGAACCATGCTTGAACCATGCTTGAAC 629
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492 ACAACATGTTTACACCATTTTCAACCATGCTTGAACCATGCTTGAACCATGCTTGAAC 551
750 TCGACACCTGTCGAAGCTTGAATTTCCGTTACCTCCGGAATGGAATTAATCATG 809
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810 TCTGCACTGATGCTCTCTTCAACCATGCTTGAACCATGCTTGAACCATGCTTGAAC 869
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870 AATACAGGCAAGTTCATGATTTGAACCATGCTTGAACCATGCTTGAACCATGCTTGAAC 929
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912 TGT 971
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1290 AGT 1344
1092 AGT 1146

RESULT 15

US-09-170-331-3
Sequence 3, Application US/09170331C

Patent No. 6028175
GENERAL INFORMATION:

APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.

TITLE OF INVENTION: A No. 6028175el Mammalian Methadone-Specific Opioid Receptor
TITLE OF INVENTION: Gene and Uses

FILE REFERENCE: 93-311-C
CURRENT APPLICATION NUMBER: US/09/170,331C
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.0

SEQ ID NO 3
LENGTH: 1452

TYPE: DNA
ORGANISM: Rattus norvegicus

FEATURE:
NAME/KEY: CDS

LOCATION: (182)..(1282)
US-09-170-331-3

Query Match 22.5%; Score 361.8; DB 5; Length 1452;
Best Local Similarity 60.6%; Pred. No. 2e-87;
Matches 616; Conservative 0; Mismatches 392; Indels 9; Gaps 1;

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 20:19:33 ; Search time 1825.6 Seconds
(without alignments)
3851.777 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 segs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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6	1167.8	72.5	1203	11	AF286024
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1610) Mester,A., Hurley,J.H., Bye,L.S., Campbell,A.D., Chen,Y., Tian,M., Liu,J., Schulman,H. and Yu,L.
TITLE	The human mu opioid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C
JOURNAL	J. Neurosci. 15 (3), 2396-2406 (1995)
MEDLINE	95198115
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Qy	1501	AGGTTGCTTCAAGATGTGT	ATGAGAGGCTCTAATTTCT	TAGAGAAATGCTGCTTTTAGGT	156
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DEFINITION	Sequence 7 from Patent W0983937.			PAT	22-JAN-2000
ACCESSION	A87781				
VERSION	A87781.1	GI:6736383			
KEYWORDS					
SOURCE		unidentified.			
ORGANISM		unclassified			
REFERENCE		1 (bases 1 to 2162)			
AUTHORS		Hoehle, M. and Wendel, B.			
TITLE		GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE VARIANTS: POLYMORPHISMS AND MUTATIONS THEREOF			
JOURNAL		Patent: WO 983937-A-06-AUG-1998;			
FEATUES		HOEHE MARGRET (DE); WENDEL BIRGIT (DE)			
SOURCE		Location/Qualifiers			
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QY	88	CGCTCCCTCTCTTCACAGCCAGACAGCTGTTTGTGAAGAAACAGCAGAGCTGTGGCAGC	147	
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QY	387	CGGACCTGGGGGGGAGAGACAGCCTGTGGCTTCCGACCGGCAAGTCCCTCATGATACGG	446	
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QY	447	CCATCCAGATCATGAGGCGCTCTACTCATGCTGTGGGTGGGGGCTCTCGGAAACTTCG	506	
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QY	507	TGGTCATGATGTGATTGTGCAGATACACCAAGATGAAGACTCCCAACCAATCTACATT	566	
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RESULT 3
HOMOMORIX 2162 bp mRNA PRI 08-AUG-1994
LOCUS Human mu opiate receptor (MOR1) mRNA, complete cds.
DEFINITION L25119
ACCESSION L25119.1 GI:452072
VERSION 1
KEYWORDS Mu opiate receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2162)
AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A.
and Uhl,G.R.
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 94139928
FEATURES
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Location/Qualifiers
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1/31/94

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DB	909	CTGCGTGAAGATCTGTGTTTTTCATCTTCGCCCTTATTAATGCCAGTGCATCATTAACCGTG	968		
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DB	969	TGCTATGAGCTATGATCTTGGCGCTCAAGAGTGCAGTGCCTCTGGCTCCAAAGAA	1028		
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QY	1115	GTCTGTGAGCTATCCATTCATCATTTACGTCATCATTAAGACCTTGGTGTAAATCCAGAA	1174		
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DEFINITION	Human mu opioid receptor variant (MOR1) mRNA, complete cds.				
ACCESSION	U12569				
VERSION	U12569.1	GI:607911			
KEYWORDS	.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 1473)				
JOURNAL	Bare, L.A., Mansson, E. and Yang, D.				
MEDLINE	Expression of two variants of the human mu opioid receptor mRNA in				
REFERENCE	SK-N-SH cells and human brain				
AUTHORS	FEBS Lett. 334 (2), 213-216 (1994)				
TITLE	2 (bases 1 to 1360)				
REFERENCE	Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffn, C.A.				
AUTHORS	and Uhl, G.R.				
TITLE	Human mu opiate receptor. cDNA and genomic clones, pharmacologic				
	characterization and chromosomal assignment				

FEATURES	source
JOURNAL MEDLINE REFERENCE	FEBS Lett. 338 (2), 217-222 (1994)
AUTHORS	94139928
TITLE	3 (bases 1 to 1473)
JOURNAL	Bare, L.A.
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QY 1303 AACCTTCCACATTTGAGACAAACAACTCCAGTGAATTCGTGAGAACTAGAGACCA 1362
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Db 1321 CCGCTCAGCGCCCAATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1371

RESULT 5
LOCUS PIGMOOPR 1881 bp mRNA MAM 03-MAR-1999
DEFINITION Sus scrofa mu opioid receptor mRNA, complete cds.
ACCESSION L38645
VERSION L38645.1 GI:2072391
KEYWORDS SOURCE
ORGANISM
Sus scrofa
Pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1881)
AUTHORS Rumpus, M.S., Osinski, M.A., Brown, D.R. and Muraugh, M.P.
TITLE The porcine mu opioid receptor: molecular cloning and mRNA
distribution in lymphoid tissues
J. Neuroimmunol. 90 (2), 192-198 (1998)
99032385
MEDLINE 2 (bases 1 to 1881)
REFERENCE Osinski, M.A.
AUTHORS Direct Submission
TITLE Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology,
JOURNAL University of Minnesota, St. Paul, MN 55108, USA
COMMENT On May 6, 1997 this sequence version replaced gi:1553056.
FEATURES
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/product="mu opioid receptor"
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LEAFATLP."
BASE COUNT 463 a 533 c 423 g 462 t
ORIGIN
Query Match 78.1%; Score 1258; DB 3; Length 1881;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1425; Conservative 0; Mismatches 175; Indels 12; Gaps 5;
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QY 64 CTCAGCTGGTCCCTCGGCTGACGCTCTCTCTGTCTAGCCAGAGACTGGTTCTGTA 123
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Db	118	AGAAATATTCACAGACCCGTGGCGGGGGCTGGAGGAAACGGGCTGAGGGCGCTGGAAACCCGAA	177
QY	184	AAGTCGTGTCCTCTTGGTACCTCGCAGCAGCGTGGCC---GCCGGGCGGTCACTAGCA	239
Db	178	AAGCCGGGTGATGGCGGTTACCTCACTGGGTGTGCCAAGCCGCGACGGCGTCACAGCA	237
QY	240	TGGACAGCAGCGCTGCCCCACGAAAGCCACGAAATTCACACTGATGCTT--GGCTACT	296
Db	238	TGGACAGCAGCGCTGACCCCCGAAAGCCACGAAATTCACACTGATGCTTCCCTCTGGCCCTTT	297
QY	297	CAAGTGGTCCCGAAGCAACGACCGCGGGTTCGGGGTCAACTGGTCCCACTTAAGATGGCA	356
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Db	358	ACCTGTCCGACCCATGCAATTGCGAACCGCACAGCAAGCTGGGGGAGAGACAGCTGTGTC	417
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Db	418	CTCCGACCCGCACTGCTCCATGATCAGCGGCATCACATATGGCCCTCTACTCATCG	477
QY	477	TGTGGTGGTGGGCTCTTGGGAAACCTCTGGTCAATGATGATTTGCAATACACA	536
Db	478	TGTGGTGGTGGGCTCTTGGGAAACCTCTGGTCAATGATGATTTGCAATACACA	537
QY	537	AGATGAGACTGCCACCAACATCTACATTTTCAACCTGCTGGCAGATGGCTTAGCA	596
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QY	597	CCAGTACCCCTCCCTTCAGAGTGTGAATACCTAATGGGAACATAGCCATTGGAAACA	656
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QY	657	TCCTTTGGCAAGATAGTATCTCCATAGATTACTATAACTGTTCCACCACATATTACCC	716
Db	658	TCCTGTGGCAAGATAGTATCTCCATAGATTACTATAATGTTCCACCACATATTACCC	717
QY	717	TCTGACCATAGAGTGTGATGATGATACACTTCGACTTCGCAACCTGTGCAAGGCTTAGAT	776
Db	718	TCTGACCATAGAGGTGTGATGATGATACACTTCGCGCTGCGCATCCCGTCAAGGCGCTGAGCT	777
QY	777	TCCGACTCCCGCAAAATGCAAAATTTTCATGTCGAACTGAGATCCCTTTAGCA	836
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QY	897	CAGTACATTTCTTCATGCAACCGGTGAGTGGGAAACCTGCGAAGATCTGTGTTTCA	956
Db	898	CAGTACATTTCTTCATGCAACCGGTGAGTGGGAAACCTGCTGAAATCTGTGTTTCA	957
QY	957	TCTTCCGCTTCATTATGCCAGTGTCTATCTACGCTGTGCTATGAGCAGTATGATCTTGC	1018
Db	958	TCTTCCGCTTCATGATCGTGTCTCTCATCTATACAGTGTGTTATGGCGTATGATCTTAC	1017
QY	1017	GCGTCAAGAGTGTCCGATGCTCTGTGGCTTCCAAAGAAAGGACAGGAATCTTCCAGAA	1076
Db	1018	GCGTCAAGAGTGTTCGATGCTCTGTGGCTTCCAAAGAAAGGATTAAGAACTGTCCAGAA	1077
QY	1077	TCACCAAGATGTGCTGTGGTGGTGGCTGTGTTCACTGCTGTGAGACTCCCATTTACA	1138
Db	1078	TCACCAAGATGTGCTGTGGTGGTGGCTGTGTTCAATGTGCTGTGAGACTCCCATTTACA	1137
QY	1137	TTTACGTATCATTAAGCCTTGTTTACAATCCCAAGAACTAGTCTCAGACTGTTCTT	1198
Db	1138	TTTACGTATCATTAAGCCTTGTTTACAATCCCAAGAACTACTTTCCAGACTGTGCTCT	1197

QY	1197	GGCACTTCTGCATTCCTCTAGATTACAAACAAAGCTGGCTCAACCCAGTCTTTATGCAT	1255
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QY	1257	TTCTGGATGAAACCTTCAACAGATGCTTCAGAGAGTTCGTATCCCAACCTTTCACACA	1316
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QY	1317	TTGAGCAACAAACCTCCACCTCGAATTGGTTCAGAACACTAGAGACCACCTCCACAGGCCA	1376
Db	1318	TTGAGCAACAAACCTCCGCTCGAATTCCTCCAAACACACAGAGACCACCTCCACAGGCCA	1377
QY	1377	ATACAGCTGGATAGAACTATCATCTACGCTAGAAAATCTGGAAAGCAAACTGCTCCGTTGC	1436
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Db	1498	GAAGCAGGTTGGCTTCAAGATGTGTAGAGAGGCTTAATTCTCTAGAAAAGTGCCTGCTT	1557
QY	1556	TAGGTATTCACCAACTCTTTCTCTCTGTGGCCACTGTGCTCTGTGCACATTGAGAG	1607
Db	1558	GA-TGTCACTAAATCTGTTCCTCTCTGTGGCGCTGTGCTCTCACACTGAGAG	1608

RESULT	6
LOCUS	AF286024
DEFINITION	Macaca mulatta mu opioid receptor mRNA, complete cds.
ACCESSION	AF286024
VERSION	AF286024..1 GI:9664878
KEYWORDS	.
SOURCE	rhesus monkey.
ORGANISM	Macaca mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca. Miller,G.M. and Madras,B.K. 1 (bases 1 to 1203) Miller,G.M. and Madras,B.K. Cloning of the Macaca mulatta mu opioid receptor Unpublished 2 (bases 1 to 1203) Miller,G.M. and Madras,B.K. Direct Submission Submitted (11-JUL-2000) Neurochemistry, New England Regional Primate Research Center, Harvard Medical School, One Pine Hill Drive, Southborough, MA 01772, USA Location/Qualifiers 1..1203 /organism="Macaca mulatta" /db_xref="taxon:9544" /tissue_type="striatum" 1..1203 /codon_start=1 /product="mu opioid receptor" /protein_id="AAP97249.1" /db_xref="GI:9664879" /translation="MDSSAVPTVNSCTDLAHSSCPARSPGSWNLSHLDGNLSDP CGPRDIDGLGRDSCLPPTGSGPSMTATITIALYSIVCVLFQNFIVMYIVRYTKK TATNITFENLADALVTSTLPDSOYVLMGTWPFGITLKIVISIDYNNMTSIFPL CTMSVDRIAYCHPVKALDERTPRNAKIIVNCNMISSLGDPVMEATYRKROGSD CTLHSRSMWTMLTKICVFETAFIMIPVLIIYVCIGILMLTLRSKVMSGSEKDN LRRTIRVLYVAAYFIICMPPIYVIYIKALKNTIPETPTQSVSHHCIALGYNSCLN PVALTFIDENKRCFFRECIPITSNIIDQNSTRLRONTKHPSIANTVDTNPQLENL EAETAPLP"
BASE COUNT	299 a 350 c 242 g 312 t
ORIGIN	

Query Match 72.5%: Score 1167.8; DB 11; Length 1203;
 Best Local Similarity 98.2%; Pred. No. 1e-293;
 Matches 1181; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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 QY 359 CTGCGCAGCCATCGGTCGCAACCGCAGCAGCTGGGCGGAGAGACAGCGCTGCGCT 418
 121 CTGCGCAGCCATCGGTCGCAACCGCAGCAGCTGGGCGGAGAGACAGCGCTGCGCT 180
 QY 419 CCGACCGGAGTCCCTCATGATGATCAGGCGCATCAGATGAGCCCTCTACTCATGCTG 478
 181 CCGACCGGAGTCCCTCATGATGATCAGGCGCATCAGATGAGCCCTCTACTCATGCTG 240
 QY 479 TGGCTGGTGGGGCTCTTCGGAACTTCTGCTGATGATGATGATGATGATGATGATG 538
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 QY 539 ATGAGAGCTGCGACCAACATCTACATTTTCAACCTTGGCTGGAGATGCTTGGCCACC 598
 301 ATGAGAGCTGCGACCAACATCTACATTTTCAACCTTGGCTGGAGATGCTTGGCCACC 360
 QY 599 AGTACCTGCCCTTCAGAGTGTGAATTAACCTTAATGGGACATGGCCATTGGAACCATC 658
 361 AGTACCTGCCCTTCAGAGTGTGAATTAACCTTAATGGGACATGGCCATTGGAACCATC 420
 QY 659 CTTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
 421 CTTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 719 TGCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
 481 TGCACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
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 541 CGTACTCCCGAATGCGCAAAATTAATCAATGCTGCAACCTGCTCTTCAAGCCATT 600
 QY 839 GGTCTCTGTAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
 601 GGTCTCTGTAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 899 CTACATTTCTCTATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
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 QY 1439 TAA 1441
 Db 1201 TAA 1203

RESULT 7
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 LOCUS BTU89677 1415 bp mRNA MAM 11-JAN-2000
 DEFINITION Bos taurus mu opioid receptor mRNA, complete cds.
 ACCESSION U89677
 VERSION U89677.2 GI:4521325
 KEYWORDS
 SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovine; Bos.
 REFERENCE
 1 (bases 1 to 1415)
 Simon, E.J., Andria, M.L., Villm, F.S., Hiller, J.M. and
 Simon, E.J.
 TITLE The bovine mu-opioid receptor: cloning of cDNA and pharmacological
 characterization of the receptor expressed in mammalian cells
 JOURNAL Brain Res. Mol. Brain Res. 73 (1-2), 129-137 (1999)
 MEDLINE 20050861
 REFERENCE
 2 (bases 1 to 1415)
 Simon, E.J., Villm, S., Andria, M., Onopriushvili, I. and Hiller, J.M.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-1997) Psychiatry, NYU Med. Center, 550 First
 Ave., New York, NY 10016, USA
 REFERENCE
 3 (bases 1 to 1415)
 Simon, E.J., Villm, S., Andria, M., Onopriushvili, I. and Hiller, J.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-1999) Psychiatry, NYU Med. Center, 550 First
 Ave., New York, NY 10016, USA
 REMARK
 COMMENT Sequence update by submitter.
 On Mar 26, 1999 this sequence version replaced gi:1881730.
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BASE COUNT 337 a 430 c 309 g 339 t
 ORIGIN

Query Match 70.8%; Score 1139.6; DB 3; Length 1415;
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 Matches 1267; Conservative 0; Mismatches 134; Indels 7; Gaps 4;

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 BASE COUNT 562 a 608 c 489 g 570 t
 ORIGIN

Query Match 69.7% Score 1122: DB 12: Length 2229;
 Best Local Similarity 83.4% Pred. No. 9.5e-282;
 Matches 1324: Conservative 0: Mismatches 255; Indels 9; Gaps 4;

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RESULT 10
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
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 SOURCE
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 1586)
 Chen Y., Mestek A., Liu J., Hurley J.A. and Yu L.
 Molecular cloning and functional expression of a mu-opioid receptor
 from rat brain
 Mol. Pharmacol. 44, 8-12 (1993)
 JOURNAL
 MEDLINE
 FEATURES
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 1. 1586
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 Qy 1228 CAGTGGCTCAACCGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1287
 Db 1194 CAGTGGCTCAACCGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1253
 Qy 1288 AGATGCTGATCCCAACGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1347
 Db 1254 AGATGCTGATCCCAACGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1313
 Qy 1348 GAACACTAGACACCGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1407
 Db 1314 GAACACTAGACACCGCTTCTGATGCTAGGTACAAACCTTCAAGCGCTTCTGAT 1373
 Qy 1408 AAATCTGGAAGCAAACTGCTGCTGCTTACAGGCTTCAAGCGCTTCTGATGCTAG 1467
 Db 1374 AAATCTGGAAGCAAACTGCTGCTGCTTACAGGCTTCAAGCGCTTCTGATGCTAG 1433
 Qy 1468 ACCAAGCTTAGAA 1480
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 LOCUS RATMOP10ID 1401 bp mRNA ROD 24-JAN-1994
 DEFINITION Rat mu op1oid receptor mRNA, complete cds.
 ACCESSION L22455.1 GI:437671
 VERSION 122455.1
 KEYWORDS mu op1oid receptor;
 SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
 ORGANISM Rattus norvegicus;
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1401)
 AUTHORS Thompson, R.C., Mansour, A., Akil, H. and Watson, S.J.
 TITLE Cloning and pharmacological characterization of a rat mu op1oid
 JOURNAL receptor
 MEDLINE Neuron 11 (5), 903-913 (1993)
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 ETAPLP
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ACCESSION	L20684
VERSION	L20684.1 GI:409149
KEYWORDS	Mu opiate receptor.
SOURCE	Rattus norvegicus [library: lambda ZAP (Stratagene)] cortex cDNA to

ORGANISM	Rattus norvegicus; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 2135)
AUTHORS	Wang, Y.-B., Imai, Y., Epler, M. C., Gregor, P., Spiyak, C. and Uhl, G. R.
TITLE	Mu opiate receptor: cDNA cloning and expression
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234 (1993)
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FEATURES	Location/Qualifiers
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ORIGIN				

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Best Local Similarity	84.7%	Pred. No. 3.5e-258		
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 20:23:20 ; Search time 87.29 Seconds
(without alignments)
6928.823 Million cell updates/sec

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Scoring table:
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Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1561	97.0	2162	19	V61985 Human mu oploid re
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6	1561	97.0	2162	19	V61987 Human mu oploid re
7	1561	97.0	2162	19	V61988 Human mu oploid re
8	1561	97.0	2162	19	V61989 Human mu oploid re
9	1561	97.0	2162	19	V61990 Human mu oploid re
10	1561	97.0	2162	19	V61991 Human mu oploid re
11	1561	97.0	2162	19	V61992 Human mu oploid re
12	1561	97.0	2162	19	V61993 Human mu oploid re

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20	1110.4	69.0	1610	21	Z60741 CDNA encoding murI
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26	924	57.4	1334	21	Z60728 CDNA encoding murI
27	924	57.4	1729	21	Z60734 CDNA encoding murI
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33	443.2	27.5	1821	15	Q56700 Mouse delta opiate
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35	443.2	27.5	2272	16	Q75927 DNA encoding a mu3
36	441	27.4	441	20	X59781 Human kappa oploid
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38	434.8	27.0	1143	18	T90998 Human kappa oploid
39	434.8	27.0	1284	18	T90999 Human kappa oploid
40	416.4	25.9	1408	19	V49254 Mouse kappa opiate
41	416.4	25.9	1410	16	Q75926 Mammalian kappa op
42	412.8	25.5	2481	16	Q86725 Murine delta opiol
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ALIGNMENTS

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XX 20-OCT-1995 (first entry)
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XX KW
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XX OS
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XX 13-SEP-1993; 33US-0120601.
XX
XX (INDV) UNIV INDIANA FOUND.
XX
XX Yu L;
XX WPI: 1995-131351/17.
XX P-PSDB: R71966.
XX
XX New nucleic acid encoding new human mu oploid receptor - and
XX related vectors, transformed cells, antibodies etc., useful in

QY	1	CGAGTGAAGCCCTGTGAACACTAATGAAGTGGAGGGGGCTATTACGACAGAGGAAATGACG	60
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Db 1321 agaacactagagaccacccctccacagccatacagtgatagaaactaatcatcagct 1380
Qy 1407 AAATTCGAGAGCAAACTCTCCGTTGCCCTTACAGAGGCTCTCATGCTTCCGACTT 1466
Db 1381 aaatctggaagcagaacctcctcgtgtccctcaagaggtctcctcctcctcctc 1440
Qy 1467 CACCAAGCTTGAAGCCACATGATGTGAAGAGAGTGTGCTTCAAGATGTGTGAGAG 1526
Db 1441 caccagacttagaagccacatgtcatgtggaagcaggtgtgtcctcaaatgtgtaga 1500
Qy 1527 CTCTAATTCCTAGAAAGTCTGCTTTTGTAGTCAATCAACCTCTTCTCTGTGCGCA 1586
Db 1501 ctctaattctctagaaagtgtcctacttttagtcatcacaacctcttctcctctg 1560
Qy 1587 CTCTGCTCTGCACATTAAGG 1607
Db 1561 ctctgctctgcacattagag 1581

```

RESULT 4
V61985
ID V61985 standard; cDNA; 2162 BP.

XX V61985;
XX
XX
XX 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 1.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX Homo sapiens.
OS Synthetic.
XX

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FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /**tag= a
FT FT /product= "mu-opioid receptor"
FT FT misc.feature 502..503
FT FT /**tag= b
FT FT /note= "Site of intron 1"
FT FT misc.feature 855..856
FT FT /**tag= C
FT FT /note= "Site of intron 2"
FT FT misc.feature 1376..1377
FT FT /**tag= d
FT FT /note= "Site of intron 3"
FT FT mutation 41
FT FT /**tag= e
FT FT /note= "Wild type G is replaced by T"
PN WO983937-A2.
PD 06-AUG-1998.
XX 02-FEB-1998; 98WO-DE00382.
PF 03-FEB-1997; 97DE-1003925.
PR (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PA Hoehe M, Wendel B;
PI WPI: 1998-437487/37.
DR
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 41 of the wild-type sequence represented in
CC V61984 is replaced by a T. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly additive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmacological agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
XX
SO Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 2 other;

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Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 28 TGGGAGGGGCTATAGCAGAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 87
Db 1 tgggaaggggctatacagcagaggaatgtcagatcctcgtgtccctcccgctga 60
Qy 88 CGCTCCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
Db 61 cgcctctctgtctcagcagagactgtttctgtaagaacagcagagactgtgtgagc 120
Qy 148 GCGCAAGAGAGCGCGCTGAGCGCTTGAACCCGAAAGTCTGCTGCTGCTGCTGCT 207
Db 121 ggcgaagagagcgctgagcgctgtgaaacccgaaagctcgtgtgtctcctgtact 180

[illegible]

Db	1261	gagagtcctgtatcccaactctctccaacattgagaaacacccacctcgtatctgct	1320
Qy	1347	AGAACTAGTAGACACCCCTCCACGGCCCAATACAGTGTATGAACATACTATCATCAGCTAG	1406
Db	1321	agaaactatgagaccacccctccacgccaatatacagttgatatagaactaatcatcagctag	1380
Qy	1407	AAATCTGGAAGACGAACACTGCTCCCTTTCCTTACAGGGGTCTATGTCATCTTCGACTT	1466
Db	1381	aaatctcggaagaagaacactgctccgttgccttaacaggtctctatgcattccgacctt	1440
Qy	1467	CACACACTTAGAAGCCACCATATATGTGAAGACAGTGTCTTCAGAATGTAGAGAG	1526
Db	1441	caccaagctttagaagccaccatgtatgtgaaagcaggttgcctcaagaatgtctagaggt	1500
Qy	1527	CTCTAATCTCTTAGAAGAAAGTGCTGCTTTTAGTGATCCAACCTGTTTCTCTGCGCA	1586
Db	1501	ctctaattctctagaaagtgacctactttagtcatccaacctctctccctctcgca	1560
Qy	1587	CTCTGCTCTGCACATTAGAG	1607
Db	1561	ctctgcctctgcacattagag	1581

RESULT	5	
V61986		V61986 standard; cDNA; 2162 BP.
XX		
AC	V61986;	
XX		
DT	11-JAN-1999 (first entry)	
XX		
DE	Human mu-opioid receptor cDNA variant 2.	
XX		
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;	
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;	
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;	
KW	cocaine; inherited alcoholism; human; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	213..2040
FT		/*tag- a
FT	misc_feature	/product= "mu-opioid receptor"
FT		502..503
FT		/*tag- b
FT	misc_feature	/note= "Site of Intron 1"
FT		855..856
FT		/*tag- c
FT		/note= "Site of Intron 2"
FT	misc_feature	1376..1377
FT		/*tag- d
FT		/note= "Site of Intron 3"
FT	mutation	80
FT		/*tag- e
FT		/note= "Wild type C is replaced by T"
XX		
PN	W09833937-A2.	
XX		
PD	06-AUG-1998.	
XX		
XX	02-FEB-1998;	98MO-DE00382.
XX		
PR	03-FEB-1997;	97DE-1003925.
XX		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
PI	Hoehe M, Wendel B;	
XX		
DR	WPI; 1998-437487/37.	
XX		

PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8, Page -: 26pp; German.

PS Claim 8; Page -; 26pp; German.

CC This sequence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 80 of the wild-type sequence represented in
CC V61984 is replaced by a T. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification

CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.

Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match	97.08	Score 1561	DB 19	Length 2162
Best Local Similarity	99.68	Pred. No. 0		
Matches 1575	Conservative	0	Mismatches 5	Indels 1
				Gaps 1

OY	28	TGAGAGGGGGCTATACCGACGAGGAGAGATGCATGATGCTGACCTGGTCCCTCCGCGCTGA	87
Db	1	ctggagagggggtctaacacgcagagaggaagatcagatgtccagctcgtctccctccgccttga	60
OY	88	GGCTCCTCTCTGCTGTCAAGCCAGGAGCTGGTTCTGTAAAGAAACACAGAGAGCTGTGGCAGC	147
Db	61	cgctccctctcgtctccagctagagactggtttcttgaagaacacagcagagagctgtggaagc	120
OY	148	GGCGAAGGAACGGGCTGTAGGCGCTTGGACCCGAAAAAGTCTCGGTGCTCTTGCTTACT	207
Db	121	ggcgaaagaagcgcgtctgagcgcgttggaaacccgaaaaagtcgtggtctcgtctgaact	180
OY	208	CGCAGACG - GAGCCCGCCCGGCGCGCTCACTATACATGAGACAGACAGCGCGTCCGCCACGAAAG	266
Db	181	cgcacagacggttgccgcgcgcgcgcgttcaatcacaatggaagaagagcgtcgcccccaagacg	240
OY	267	CCAGCAATTTGCATGATGCTCTGGCGGTACTCAAGTTGTCTCCCAAGCACCCAGCCCGGTT	326
Db	241	ccagaaatgtacatgactgctgtgcgtactcaagtgtctcccaagaacccagccccggtt	300
OY	327	CCTGGGTAACTTGTGCCACTTAGATGGCAACTGTCCGACCCTAGCGGTGCCAACCGCA	386
Db	301	cttggttcaactgttcccaacttaagtggcaaacctgtccgaccacatgctgcgcgaacgcga	360
OY	387	CCGACCTGGGGGGGAGACAGACGCTGCTCCCTCCGACCGGAGAGTCCCTCCATATGATCAAG	448
Db	351	ccaacctggcgggagagagacacgctgtgacctccgaaccgagctccctcatgtatcaag	420
OY	447	CCATCAGCATATGGCCCTCTACTCCATCATGTCGTGCGTGTGGGGCTCTTGGAAACTTCC	506
Db	421	ccatcagcatcatgtgcccctctaccctacatcgtgtggtggtggtctcttctggaacttcc	480
OY	507	TGGTCATATATGTATTGTCAGATATACCAAGATGAGACATGCCACCAACTTCTACATT	566
Db	481	tgttaattatgtatgtatgttgcagatacaccaagaatgaaagacgtgcacacaactctacat	540
OY	587	TCAACCTGCTCTGGCAATGCTCTTAGCCACACAGAACCTGCTCCCTCCAGATGTGATT	626
Db	541	tcaacctgtctcgtgcgaatgctcttaggcacacagtaacctgtcccttccagaagtgtgaat	600
OY	627	ACCTAATGGAAACATGGCCATTTTGGAACCACTCTTTGCACAGATAGTACTCCATAGATT	686
Db	601	acctaatggaaacatgagcatttggaaacatcctttggaatatgtaacttccataat	666

QY	687	ACTATACATGTTACACAGATATTACCCCTGTGCACCACTAGTGTTGATGATACATG	746
Db	661	actataacatggttaccacagatattacccctgtgcacacatggttgcatacatcttg	720
QY	747	CAGTGTGCACCCGTCAAGCGCTTGATGTTCCGTACGTCCCGAATGCGAAATTATCA	806
Db	721	cagtcgtcacccgttcaaggccttgcattccgtactcccgaaatgcccataatcatca	780
QY	807	ATGTCTGCAAATGTGATCCTCTTCTTACAGCATTGGTCTTCCCTTAATGTTAC	866
Db	781	atgtctgcaactgtgatcctctcttcacgcatctgtctctgtaatgltcatgcttaaca	840
QY	867	CAAAATACAGGCAAGTTCATAGATTGTACATTAACATCTTCTATCCAACTGTGACT	926
Db	841	caaaatacaggcaaggttcataagattgtacatacaatcttcataccaacctgtaact	900
QY	927	GGGAAACCTCTGCAATATGTGTTTATCATCTGCGCTTCAATGCGACAGTCATCA	986
Db	901	gggaaacctctgtaagaatctgtttcaatcttgccttcataatgccagtgctcatca	960
QY	987	TTACCGTGTGCTATGACATGATGATCTTGCGGCTCAAGAGTCCGACGTCTCTGGCT	1046
Db	961	ttaccgtgtgtatgacatgatgatctgtgcgtcaaggtgtccagatgctctctgtcgt	1020
QY	1047	CCAAAGAAAGAGACAGAAATCTTCGAAGGATCACCAAGATGCTGCTGGTGGTGGCTG	1106
Db	1021	ccaaagaaagagaaagaaatcttcgaaggatcaaccagatgtgtgtgtgtgtgtgtgt	1080
QY	1107	TGTTATCGTGTGCTGTGACATCCCATTCACATTAATGATCATCTTAATTAACCTGGTTACAA	1166
Db	1081	tgttatcgtgtgtgtgtgacatcccatcacaattagatcatcatataagccttggttaaaa	1140
QY	1167	TCCAGAAACTACGTTCCAGATGTTCTTGGCACTTCGTGCAATGCTCTAGGTTACACAA	1226
Db	1141	tccagaaacctacglttccagatgtttcttcttggaacttcgtcatgtctctaggttaacaaa	1200
QY	1227	ACAGCTGCTTCACACCCAGTCTCTTATGCAATTTCTGATGAATAACTTCAAGAGTCTTCA	1286
Db	1201	acagctgtccttaaccacagltccttlatgtcattcttgatgaataacttcaaaagatgtctca	1260
QY	1287	GAGAGTTCTGTATCCCAACCTCTTCCACATTGAGCAACAAACTCCACTGGAATTCGTC	1346
Db	1261	gagagttctgtatcccaacctcttccaacattgagaaacaaacctccactcgaattgtctc	1320
QY	1347	AGAACACTAGAGACACCCCTCCAGCGGCAATACACTGATGAAGAACTAATCATCAGCTAG	1406
Db	1321	agaacactagagaccacccctccacgccaataacagttagatagaactaatcatcagctag	1380
QY	1407	AAATCTGGAAGCGAAATCGTCCGTTGCCCTAACAGGCTGTCAATGGCATTTCGACACTT	1466
Db	1381	aaaactctggaagcgaaactgctccgttgcctcaaaaggtcttcacatccatccgaactt	1440
QY	1467	CACCAAGCTTAGAGCCACCATGATGATGGAAGACAGTGTCTTCAGAAATGTTAGAGAG	1526
Db	1441	caccaagcttagaagccacacatgtagtgaagcaggttgcctcaagaatgtgttagagag	1500
QY	1527	CTTAAATCTGTAGAAATGTCCTTTTAAAGTCAATCCACTCTTTCTCTCTGTGACCA	1586
Db	1501	cttcaatctcttagaagaagtgcttaacttttagtcatccaacctcttcctctctgtgcca	1560
QY	1587	CTCTGCTCTGTACATTAGAGG 1607	
Db	1561	ctctgctctgtcacatitagagg 1581	
RESULT	6		
AC	V61987		
AC	V61987	standard, cDNA, 2162 BP.	
XX	V61987;		
XX	11-JAN-1999 (first entry)		

RESULT	6	.
V61987		
ID	V61987	standard; CDNA; 2162 BP
XX		
AC	V61987;	
XX		
DT	11-JAN-1989	(first entry)

Query Match	97.0%	Score 1561	DB 19	Length 2162
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1575	Conservative 0	Mismatches 5	Indels 1	Gaps 1

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D	b	1	tgaggagggggtatacgcagaggaagaatgacagatgctcagctcggctccctccgctga	60
Q	y	88	CGCTCTCTCTGTCTACGCCAGACTGTTTCTGTAAAGAACAGCAGAGCTGTGGCAGC	147
D	b	61	cgctccctcctgctccagccaagactggtttctgtatagaataagacgagacgtgtgcagc	120
Q	y	148	GGCGAAAGGAAGCGCGCTGAGAGCCCTTGGAACCCGGAATAATCTCGGAGCTCGCTACTT	207
D	b	121	ggcgaagaagaaagcgcgcgagcgctcggaaaccggaaagatctcgtgtgctccgtgtaact	180
Q	y	208	CGCACAGC-GTGGCCGCCGCCGCGTCAGTACATGAGACAGACGCGTGCCTCCACGAACG	266
D	b	181	cgcaacagcgtgtcccgccgcgcgctcagtaaccaatgacagcagcgtgtgcctccacgaacg	240
Q	y	267	CCAGCAATGTGACAGTATGCGCTTGCGCTACCAAGTTGCTCCACAGACCCACCGGGTT	326
D	b	241	ccagaaatctgacatgacctgtgcgaaccaaagttgtccccaagaccagccccggtc	300
Q	y	327	CCTGGGTCAACTTGTCCCACTTATGATGGCAACCTGTCCAGACCATATGGGTCCGAACCGCA	386
D	b	301	ctgtggtcaactgttccactatgatgcaacctgtccgaccocatgtcgttcggaacgcga	360
Q	y	387	CCGACCTGGCGGGGAGAGACAGCCTGTGGCCTCCAGCCGGCAGTCCCTCATGATCAGG	446
D	b	361	ccaacctgtggggagagaaagacagcctgtgccttcgcgcgcgcagctccctcatgatacag	420
Q	y	447	CCATACGATCATGGCCCTTACTCCATCGTGTGCGATGGGGGCTTCGGAAACTTCC	506
D	b	421	ccaatcagatatagtgcccttactcatctgtgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgt	480
Q	y	507	TGGTCACTATGTGATGTTGAGATPACACCAAGATGAAGACTGCCACCAACATCTACATT	566
D	b	481	tggtatctatgtatgtattgataagataccaagaatgaaagactccacaacatctacatt	540
Q	y	567	TCAACCTTGGCTGGCGAGTGGCTTTAGCCACAGTACCTGGCCCTTCGAGATGTGAATT	626
D	b	541	tcaacctgtccgtgcagaaagccttgagcaaccagatcacctgcctcccaagatgtgaatt	600
Q	y	627	ACCTAATGGGAACATGGCCATTTTGGAAACCATCTTTGGAAAGATAGTATCTCCATAGATT	686
D	b	601	acctaaatgagacaatgacatttggaacacatcttgcgaagtagatctcatagatt	660
Q	y	687	ACTATACATTTTACACAGATATTACCCCTCGACACATGAGTGTGATTCGATACATTG	746
D	b	661	actataaactgttacaagataataatcaacctgcgcacatgagtgtgtgatacatatg	720
Q	y	747	CAGTGTGCACCCCTGTCAAGGCTTGTGATTTCCGTACTCCCGGAATGCCAAATTTATCA	806
D	b	721	cagttctgcacccctgtaaagccttgattctcgtactcccgaaatgcaaaatatca	780
Q	y	807	ATGTCTGCACTGGATCCCTCTTTCACGCCATTGCTTCCTGTATGTTCATGTGCTACAA	866
D	b	781	atgtctgaactgtgatactctcttcacgcaatgtgtcttccttcttaatgtcatatgatacaa	840
Q	y	867	CAAAATACAGCAAGTTCATATGATGTGTACATATCACTTCCTATCCCAACTCGTACT	926
D	b	841	caaaatacagccaaggttccatagattgtacatacaatctcccatccaacctgtact	900
Q	y	927	GGGAAAACCTGCTAAGATCTGTGTTTTCATCTTCGCTTCATTATACGAGTGCATCA	986
D	b	901	gggaaaacctcgtgaagaatctgtgttttaactcttcgcttcattatgcagatgcatca	960
Q	y	987	TTACCGTGTGTTATGACATATATCTTGCGCCTCAAGAGTGTCCGATGCTCTGGCT	1048
D	b	961	ttaccgtgtgtcatgagactgtatgactcttgycctccaagagtgtccgacatgctcttggtc	1020
Q	y	1047	CCAAAGAAAAGACAGGAATCTTCGAAGGATCCAGAGATGGGCGGGTGGGGGCGGTG	1108
D	b	1021	ccaaagaaaagacagaaatcttcgaagaatcaaccagatgtgtgtgtgtgtgtgtgtgtgtgt	1088
Q	y	1107	TGTTCAATGCTGTGCTGGACTCCCAATTCATTTACGTCACTATTAAAGCCTTGTTACAA	1166

Db	1081	tgctcaatcgtctgctgtagccatccattcaactaagtcataacttaagagcttggtacaa	1140
Qy	1167	TCCCGAAGAACTACCTTCCACACAGCTTTCTTTGGACTCTTGCAATTGCTCTAGSTTACAA	1226
Db	1141	tcccaagaactagcttccagaactglttcttgcgaacttcgcatgctcaggttacaa	1200
Qy	1227	ACAGCTGCCTCAACCCAGTCTTTATGCAATTTGTGATGAATAAAGTTCAACAGATGCTCA	1286
Db	1201	acagctgctcaaccagctccttattgaattcttgatgaaacttcaaaagatgcttca	1260
Qy	1287	GAGAGTTCTGTATCCCAACTCTTCCAACTTTAGCAATTTAGCAACAAAATCTCACTGCAATTGCT	1346
Db	1261	gagagttctgtattcccaactctctccaactctgagaacaaactccactcgaattctc	1320
Qy	1347	AGAACACTAGAGACACACCCCTCCACGCGCAATACAGTGATGAAGTAATATCATCAGCTAG	1406
Db	1321	agaagacttagagaccacccctccaagggccaatcagttgatatgaactaatctcagctag	1380
Qy	1407	AAAATCTGGAGACGAAATGCTCCGTCCGTGGCCCTAACAGGGTCTCATGCCATTCCGACTT	1466
Db	1381	aaaatctggaagcagaacactgctccgttgcgcttaacagtgcttcattgcattccgaactt	1440
Qy	1467	CACCAAGCTTAGAAGCCACCATGATGTGGGAACAGAGTGTCAAGAAATGTGTAGAG	1526
Db	1441	caccaagcttagaagccacatgtagtggaaacaggttgccttcaagaatgtagtgaag	1500
Qy	1527	CTTAATATCTTAGAAGAGTCCCTGCTTTAGGTCAATCCAACTCTTTCCTTCGGCCA	1586
Db	1501	ctctaattctctaggaagtgctactattagtgatcaccactcttctctctcgaca	1560
Qy	1587	CTCTGCTCTGCACATTAGAG	1607
Db	1561	ctctgctctgcacattagag	1581

XX	V61988	
ID	V61988 standard; cDNA; 2162 BP.	
AC	V61988:	
DT	11-JAN-1999 (first entry)	
DE	Human mu-opioid receptor cDNA variant 4.	
XX		
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;	
KW	prediction; addition; analgesic; anaesthetic; anti-addictive;	
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;	
KW	cocaine; inherited alcoholism; human; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	key	Location/Qualifiers
FT	CDS	213..2040
FT		/tag= a
FT		/product= "mu-opioid receptor"
FT	misc_feature	502..503
FT		/tag= b
FT		/note= "Site of intron 1"
FT	misc_feature	853..856
FT		/tag= C
FT		/note= "Site of intron 2"
FT	misc_feature	1376..1377
FT		/tag= d
FT		/note= "Site of intron 3"
FT	mutation	175
FT		/tag= e
PX	WO9833937-A2.	/note= "Wild type C is replaced by A"
XX		
PN		
XX	06-AUG-1998	
XD		

XX 02-FEB-1998; 98WO-DE00382.
 PF
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Hoehe M, Wendel B;
 XX
 DR WPI: 1998-437487/37.
 XX
 PF New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -: 26pp; German.

CC This sentence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 175 of the wild-type sequence represented in
CC V61984 is replaced by an A. The wild-type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
XX
XX Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other;

[illegible]

Oy	507	TGGTCATATGATGATATTTCTGCATATACACGAAGATGAAGACGGCACCAACATCTACTTT	566
Db	481	tggctcatatgatatgatatgttcgataacaccaagaatgaaagactgccaccaacatctacatt	540
Oy	567	TCAACCTGGCTCTGGCAGATGCTTAAAGCCACAGTACCTACCTGCCCCCTTCAGAGTGTGAATT	626
Db	541	tcaacctggctcttgccagatgctcttagccaccagttacccttgcccttcacagtggtgatt	600
Oy	627	ACCTTAATGGGAACATGGGCATTTTGGAAACATCCTTTGCAAGATAGTATCTCCATAGATT	686
Db	601	accttaatgggaacatgagccatttggaaacatcctttgcaagatagttatctcatagatt	660
Oy	687	ACTTAACATATGTCACCGACGATATTCAACCCCTGCACACATAGAGTGTGATCGATACTTG	746
Db	661	actataacaatgttcaacccagcatattcacccctgcacacaagaagtggtatgcataacatg	720
Oy	747	CAGTCTGCCACCCGTGTCAAGGCGCTTAGATTTCCTACTCTCCCGAATAGCCAAATATTATCA	806
Db	721	cagtctgccaccctgtctaaaggccttagatttcctgtactcccggaaatgccaataattatca	780
Oy	807	ATGTCTGCACTGGATGCTCTCTTCACGCCATGSGTCTTCTGTATGTTATGGCTACAA	866
Db	781	atgtctgcaactgatactctctcttcacgcatlgtctctctgtaattgtatcgtctacaa	840
Oy	867	CAAAATACAGGCAGAGGTTCCTACATATGTATACATACATATCTGCATACCAACCTGGTACT	926
Db	841	caaaatacagaagcaaggttccataagatgtatacaacatcttccataccaaacctggtaact	900
Oy	927	GGGAAACCTCTGTGAAGTCTGTGTATTTTCATCTTCGGCTTCATTATCCAGTGCATCA	986
Db	901	gggaaacctctgtaaggtctgtgttttcatcttcctgcctcatattatgccaagtctcatca	960
Oy	987	TTACCGTGTGCTATGAGACTATGATCTTGGCCCTCAGAGAGTGTCCGATGCTCTGSGCT	1044
Db	961	ttaccgtgtgctatgagactatgattcttggccctcagagagtgtccgactctctctgct	1020
Oy	1047	CCAAAGAAAGAGACAGGAATCTTGGAGAGATCACAGAGATGSGTSGTSGTSGTGGCTG	1104
Db	1021	ccaaagaaaggagcaggaatcttcgaagatcaccaagagaatggtctggtgtgtgtgtgtgtgt	1088
Oy	1107	TGTTTCATGTTGCTGAGACTGCCATTCCATTACATTTACGTATCATTTAAAGCCCTTGATTCAA	1166
Db	1081	tgttcatctgtctgtgagactgccatttccattacgtatcatattttaaagccttgtttacaa	1144
Oy	1167	TCCCAAGAACTAGCTTCCAGACTGTTTCTTG6CACTTGTGCAATGCTCTAG6TTACAAA	1222
Db	1141	tcccaagaactagcttccagactgttcttcttgcaacttgcattgtccttagtttacaacaa	1200
Oy	1227	ACAGTGGCTCAACCCATCCTTTATGATTTCTGMAATCTGMAAATCTTAAACGATGCTTCA	1288
Db	1201	acagctggctcaacccatcctttatgatttcttcttgcaacttgcattgtccttagtttacaacaa	1266
Oy	1287	GAGAGTTCTGTATCCCAACCTCTTTCACATTTGAGCAACAAATCTCACATCGAATTGCTC	1344
Db	1261	gagagttctgtatcccaaccttcttcttcatgatttcttgagatgaanaacttaaacagatgtctta	1322
Oy	1347	AGAACTAGAGACCCACCCCTCCACAGGCGCAATACAGTGATAGAACTAATCATCAGCTAG	1404
Db	1321	agaacactagagaccacccctccacagccaatacagatgagatgaactaatcatcatcagtag	1388
Oy	1407	AAATTCGGAAGCAGAAATCTCTCCGTTGGCCCTTAACAGGGGTCTATGCCATTCCGACTT	1466
Db	1381	aaatctcggaaagcagaaatctctccgttgccttaacagaggttctcatgtccatcccgacctt	1444
Oy	1467	CACCAAGGTTTGAAGGCCACATGTATGTGGAAGAGAGGTGGTTCAAAATAGTGAGAGG	1522
Db	1441	caccaagcttgaagccaecatgtatgtggaagcaaggttctcttaagaatcgtgtatggaag	1500
Oy	1527	CTCTAATTTCTTAGAAAAGTGCCGTGTTTATGATCAACCAACCTTTCTCTCTGTGGCCA	1588
Db	1501	ctctaatctcttagaaagtgcttacttttagtgcataccaaccttctctctctgtgcca	1566
Oy	1587	CTCTGCTCTGTGCACATTAGAGG 1607	

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Db      1561 ctcgtctgcacattagagg 1581
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RESULT      8
ID          V61989
V61989 standard; CDNA; 2162 BP.
AC          V61989;
XX
XX
XX      11-JAN-1999 (first entry)
DT
XX
DE      Human mu-opioid receptor cDNA variant 5.
XX
XX      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM      predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW      psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KV      cocaine; inherited alcoholism; human; ss.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
FH      CDS
FT      213..2040
        /location=Qualifiers
        /tag=a
        /product="mu-opioid receptor"
FT      misc_feature
        502..503
        /tag=b
        /note="Site of intron 1"
FT      misc_feature
        855..856
        /tag=c
        /note="Site of intron 2"
FT      misc_feature
        1376..1377
        /tag=d
        /note="Site of intron 3"
FT      mutation
        229
        /tag=e
        /note="Wild type C is replaced by T"
FT
FT
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      PD
XX      02-FEB-1998; 98MO-DE00382.
XX
XX      PF
XX      PR      03-FEB-1997; 97DE-1003925.
XX
XX      PA      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      PI      Hoehe M, Wendel B;
XX
XX      DR      WPI; 1998-437487/37.
XX
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
PT      used, e.g. to predict pre-disposition to addiction and for
PT      development of analgesics, anaesthetics and anti-addiction agents
XX
XX
XX      Claim 8; Page -: 26pp; German.
XX
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
CC      nucleotide at position 229 of the wild-type sequence represented in
CC      V61984 is replaced by an T. The wild type receptor and its variants,
CC      polymorphisms and mutants are used in a method for detecting
CC      predisposition to disease, particularly addictive disease, by isolating
CC      DNA from a sample, genotyping selected positions and comparing with a
CC      reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC      anti-addictive and psychopharmaceutical agents, to construct genes and
CC      vectors, particularly for pharmaceutical development, to develop
CC      diagnostic kits for predicting risk of addiction, response to analgesics
CC      or anaesthetics, or development of side effects from a drug. Particular
CC      applications are to determine risk of addiction to opiates or cocaine, or
CC      developing inherited alcoholism.
CC
CC      Note: This sequence is not represented in the specification and has

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CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX

Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

28 TGGAGAGGGGCTATACGACAGAGAAATGTAGATGCTCAGCTCGTCCCTCCGCTGA 87
 1 tggagaggggctatacgacagagaaatgtcagatgtcagctcgctccctccgctga 60
 88 CGCTCTCTCTGTCTACGACAGACTGTTTCTTAAGAAACAGACAGAGAGCTGTGGCAGC 147
 61 cgcctctctgtctcagacagagactgttctgttaagaaacaagagactgtggagc 120
 148 GCGGAAAGAGGCGGTGAGGCGCTTGAACCCGAAAGCTCGTGTCTCTGCTGCTACT 207
 121 ggcgaaagagagcgctgagcgctgtgaaacccgaaagctcggtctctctgctact 180
 208 CGCACAGC-6TGCCCGCCGCGCGCTCAGTACATGACAGAGCGCTGCCCGACGAGAGC 266
 181 cgcacagcggtgcgcgcgcgctcagtaaccatgagcagcgctgtcccgacgagc 240
 267 CAGGCAATTCGACTGATGCTTGGCGTACTCAATGTCTCCCGACGCCAGCCCGCGTT 326
 241 ccggaactgacatgactgtgctgctgactcaagtgtcccgacgacccagcccggt 300
 327 CCTGGGTCACTTGTCCCACTAGATGAGCAACCTGTCCGACCCATGCGGTCCGAAACGCA 386
 301 cctgggtcaactgtgccacttagatgtcaactcgtccgacccatgtggtccgacgca 360
 387 CGCAGCTGGGCGGAGAGACAGCCCTGTCCCTCCGACCGGAGTCCCTCATGATCAGG 446
 361 ccaactggcgagagagacagcctgtgcctccgacgagcagctccatgtagtcag 420
 447 CCATCAGATCATGCGCCCTTACTCCATCGTGTGCGGTGGGCGCTTTGGAAACTTCC 506
 421 ccatcagatcatgccccctactccatcgltggtggtggtgtctcttggaaactcc 480
 507 TGGTCATGTATGTATGTAGATGATACACAAAGATGAGACTGCGACCAACATCTACATT 566
 481 tggtcattgtatgtatgtatgatacacaagaatgaaagtgcacacaacatctacat 540
 567 TCAACCTTGTCTGGCAGATGCTTAGCCACACAGTACCTGCCCTTCCAGATGTGAATT 626
 541 tcaacctgtcttggcagatgcttagccacacagtagccttccagagtgtgatt 600
 627 ACCTAATGGGAACATGGCCATTTGGAAACATCCTTTGCAAGATAGTATCTCCATAGATT 686
 601 acctaatgggaacatggccatttggaaacatcctttgcaagatagatctccatagatt 660
 687 ACTATAACATGTTACACAGATATTCACCTTGACACATGAGTGTGATGATGATCTTG 746
 661 actataacatgttaccacagatatctccctctgcacacagagtgtgatacagatactg 720
 747 CAGTGTGCAACCTGTGCAAGGCTTAGATTCCGTACTCCCGAAATGCCAAATTAATCA 806
 721 cagtggtcacacctgtcaagccttagatttccgtactcccgaaatgcaaaatlatca 780
 807 ATGTCTGCAACTGATGATCTCTTCAAGCATGTGTCTTCTGTAAATTTATGGCTCAAA 866
 781 atgtctgcaactgatatctcttcaagcattgttcttccgttaagtgtatgtctacaa 840
 867 CAAATACAGGACGATTCATAGATGTACACTAATCATCTCTCAACCAACCTGGTACT 926
 841 caaatacagacgacgatctcatagatgtacactaaatctctcacaacctggtact 900
 927 GGGAAACCTGTGAGAGATGTGTGTTTTCATCTTGGCTTCATTATGCAAGTGTCTATCA 986
 901 gggaacacctgtgagagatgtgtgttttcattcttgccttcattatgtcagtgctatca 960

987 TTACCGTGTGCTATGAGCTGATGATCTGTGGCTCAAGAGTGTCCGATGCTCTGGCT 1046
 961 ttacggtgtctatgactgtatgtatctgtccctcaagatgttcgcagatctctcgtt 1020
 1047 CCAAGAAAGAGACAGAACTCTTGAAGATCACAGAGATGTGTGTGTGTGTGTGTGTGT 1106
 1021 ccaagaaagagacagaaactcttcgaagatcacagagatcagtggtgtgtgtgtgtgt 1080
 1107 TGTTCATGCTGTCTGTGACTCCCATTCACATTTAGTCATCATTAAGCCTTGTGAACA 1166
 1081 tgttcattgtctgtgtgactcccatcacaattagctcatcatlaaagcctgtttacaa 1140
 1167 TCCGAGAAATACAGTTCACAGACTGTTTCTTGGACTTCTGCAATTTGCTGTAGTACAA 1226
 1141 tccgagaaatactagttccagactgttcttgcactcttgcattgtcttagttacaa 1200
 1227 ACAGCTGCTCAACCCAGTCTTTATGCAATTTGTGATGAAACTTCAACAGATGCTTCA 1286
 1201 acagctgctcaacccagctctttagatcttctgtatgaaacttcaaacgtatgttca 1260
 1287 GAGAGTTCTGTATCCCAACCTTCCACATTGAGCAACAAACTCCACTGGAATTGCTC 1346
 1261 gagagtctgtatcccaactcttccaacattgagcaacaacatccactcgatctgtc 1320
 1347 AGAAGACTAGAGACACCCCTCCACGCGCCAAATACAGTGAATAACTAATCATCAGCTAG 1406
 1321 agaagactagagacacccctccacgcccatacagtgtagaactaaatcacaactag 1380
 1407 AAATCTGAGAGCAAAAGTCTCGTTCCTTAACAGAGGTCTCATGCTTCGACCTT 1466
 1381 aaatctgagagcaaaagctcgttgccttaacagaggtctcatgcttcgacctt 1440
 1467 CACCAAGCTTAGAAGCCACCATGTATGTGAGACAGAGTGTCTTCAAGATGTGTAGAGG 1526
 1441 caccagcttagaagccacatgtatgtgaagcagttgtctcaagaatgtgtagag 1500
 1527 CTCTAATTCCTTAGAAGAGGCTGTTTATGATCAATCCAACTCTTCTCTGCGCA 1586
 1501 ctctaatctcttagaagagctttagttagtcaatccaaactcttctctctgcca 1560
 1587 CTCTGCTCTGACATTAGAGG 1607
 1561 ctctgctctgacattagag 1581

RESULT 9
 ID V61990
 V61990 standard; cDNA; 2162 BP.
 XX
 AC V61990;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 6.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predisposition; addiction; analgesic; anesthetic; anti-addictive;
 KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT CDS 213..2040
 FT /tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /tag= b
 FT /note= "Site of intron 1"
 FT 855..856
 FT misc_feature
 FT /tag= c

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QY 1467 CACCAAGCTTAGAAGCCACCATGTATGTGAGACAGGTTGTTCAAGATGTAGAGAG 1526
1441 caccagcttagaagccacatgatgtggaagcaggtgtctcaagaatgtgtagagag 1500
QY 1527 CTCTAATCTCTAGGAAGTGGCTTTTAGTCATCCACCTTCTCTCTGGGCA 1586
1501 ctctaattctctagaagtgcttactttagtcatcacaacctcttctcttgacca 1560
QY 1587 CTCTGCTGCACATTAAGG 1607
1561 ctctgctctgcacattagag 1581
RESULT 10
V61991
ID V61991 standard; cDNA; 2162 BP.
XX
AC V61991;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 7.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW prediagnosis; addition; analgesic; anaesthetic; anti-addictive;
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS
XX Synthetic.
FH
FH Key Location/Qualifiers
FT CDS 213..2040
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FT /product= "mu-opioid receptor"
FT misc_feature 502..503
FT /*tag= b
FT /note= "Site of Intron 1"
FT misc_feature 855..856
FT /*tag= c
FT /note= "Site of Intron 2"
FT misc_feature 1376..1377
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FT /note= "Site of Intron 3"
FT mutation 666
FT /*tag= e
FT /note= "Wild type A is replaced by G"
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PN W09833937-A2.
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XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-DE00382.
XX
XX 03-FEB-1997; 97DE-1003925.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Hoehe M, Mendel B;
XX
XX WPI; 1998-437487/37.
XX
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX
XX
XX Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX nucleotide at position 666 of the wild-type sequence represented in
XX V61984 is replaced by a G. The wild type receptor and its variants,

CC polymorphisms and mutants are used in a method for detecting
CC prediagnosis to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmacological agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
XX
XX Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other:
50
Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 2;
QY 28 TGGAGGGGGCTATACGAGAGAGAAATGATGCTACAGCTGGTCCCTCGCCTGA 67
1 tggaggggggtatatacgagagagaaatgctacagctggctccctcgctga 60
QY 88 CGTCTCTCTGTCTACAGCCAGACTGTTCTGTAGAAACAGCAGAGAGCTGTGGCAGC 147
61 cgtctctctgtctacagccagactggttcttlaaanaacagagagctgtggcagc 120
QY 148 GGGCAAGAGAGCGGCTAGCGCTTGGAACCCAAAGTCTCGTGTCTCTGCTACT 207
121 gggcaagagagcggttagcgcttggaacccaaagtctcgtgtctctgctact 180
QY 208 CGCACAGC-GTCCCGCCCGCCGCTCACTACATGAGACAGCGCTGCCCAAGAG 266
181 cgacacagcggtcccgcccgctcagctacatgagacagcagcgtgccccaagag 240
QY 267 CCAGCAATGACATGATGCTTGGGCTACTAAGTGTGCTCCCAAGACCCCGGTT 326
241 ccagcaatgacatgactgtcttgggctactcaagtgctcccaagaccccggtt 300
QY 327 CCTGGGTCAACTTGTGCCACTTATGAGCAACGTGCGACCCATGGCGTCCGAACGCA 386
301 cctgggtcaacttgtgccacttatagcaacctgtccgaacctggttccgaacgca 360
QY 387 CGGACCTGGCGGAGAGACAGCCTGTGCTCCGACCGGAGTCCCTCATGATCAGG 446
361 cggacctggcgagagagacagcctgtgctccgacccgagtcctccatgatacag 420
QY 447 CCATCAGCATATGCGCTTACTTCATCTGTGCTGCTGGGCTCTTGGAAACTTCC 506
421 ccatacagcatatgcttacttccatcctatgctgtgtgtgtgtgtgtgtgtgtgt 480
QY 507 TGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
481 tggcatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 540
QY 567 TCAACTTGTCTGAGAGAGTGGCTTACGACAGTACCTGCTCCCTCCAGAGTGAAT 626
541 tcaacttgtctgagagagtggttaccagacagcttccctccagagtgtgaatt 600
QY 627 ACCTAATGGAACATGGCCATTTGGAAACATCTTTGAAATATGATGATGATGAT 686
601 acctaatggaaacatggccatttggaaacatctttgaaatagtatgtatccatag 660
QY 687 ACTAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
661 actaatacatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 720
QY 747 CAGTCTGCCACCTGTGCAAGGCTTGAATTTGCTACTCCCGAAATGCCAAATATCA 806
721 cagtctgccacctgtgcaaggcttgaatttgcctactcccgaaatgccaaatataca 780

DR WPI: 1998-437487/37.
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a T
CC nucleotide at position 1014 of the wild-type sequence represented in
CC V61984 is replaced by a C. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
CC
XX
SQ Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 2 other;

- Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGGAGGGGGCTATACGAGAGAGAGATGTCAGATGTCAGTCCGCTCCCTCGA 87
DB 1 tgggaaggggctatacagcagaggaagatgcatgctcagctgctccctccgctga 60
QY 88 CGCTCTCTCTGTCTCAGCCAGAGACTGGTTCTGTGAAGAACAGAGAGAGCTGGCAGC 147
DB 61 cgtctctctctctcagcagcagactggttctgtlaagaacagagagagctgtgcaagc 120
QY 148 GGGCAAGAGAGCGGCTGAGGCGCTTGGAACCCGAAAGTCTCGGTGCTCCGTGTA 207
DB 121 ggcgaagaaagagcggctgagcgcttggaacccgaagctcgtgctcctggtact 180
QY 208 CGCAGAGC-GTGCCCGCGCGCGCTGAGTACATGAGAGAGAGAGAGAGAGAGAG 266
DB 181 cgcacagagggcgcccgccgctcagctacatgagcagcagcgctgcccccaagacg 240
QY 267 CCAGCAATGCACTGATGCTGGGCTGACTCAAGTTGCTCCCGAGACCCAGCCGGTT 326
DB 241 ccagcaatgcatgactgctggtgactcaagtgctcccgagcaccccgctt 300
QY 327 CCTGGGTAACTTGTCCCACTTAAGTGGCAACTGTCCGAGCCATGCGGTCCGAACGCA 386
DB 301 cctgggtaaactgtcccaacttaagtgcaacctgtccgacccatgctcgaaacgca 360
QY 387 CCGAGCTGGGGGAGAGACAGCCTGTGCTCCGAGCGGAGTCCCTCCATGATCAGG 446
DB 361 ccaacttgggggagagagacagcctgtgctcctcgaccgagctccctcatgatacag 420
QY 447 CCATCAGCATATGAGCCCTTACTCCATGCTGTGCGTGGGGCTTTCGGAACCTTC 506
DB 421 ccatacagatcatgagccctctactccatcgtggtggtgggtctcttggaaattcc 480
QY 507 TGGTCATGTATGTATTTTCAGATACACAGATGAAGATGACACCAACTCTCATTT 566
DB 481 tggtcattgtatgtatgttccagatacacaagatgaagactgccaacatctcaattc 540
QY 567 TCAACCTGTGCTGAGCAGATGCTTACGACACAGATGCTGCGCTTCAGAGATGTAAT 626
DB 541 tcaacctgtgcttggcagatgctttagcaccagtaacctgtcccttccagagtgtgaatt 600
QY 627 ACCTAATGGAAACATGGCCATTGGAACCATCTTTGCAAGATAGTATCTCATAGATT 686

DB 601 accaatggnacatgagcattggaaccatctcttgaaagatagtgatcccatagatt 660
QY 687 ACTATATATTTTACCCAGCATATTCACCTCTGACACATAGTGTGATGATACATG 746
DB 661 actataaatatgttcaaccagcatatcacctctgcacataagatggtatgatacatatg 720
QY 747 CAGTCTGCCACCTGTCAAGGCTTAGATTCCGTACTCCCGCAAAATCCAAATATCA 806
DB 721 cagctgtcacccgttcaagccttagatttcgtactccccgaatgccaattatca 780
QY 807 ATGTCTGCAATGGATCTCTCTTCAAGCATGTGCTTCTGTATGTTCATGGCTACAA 866
DB 781 atgtctgaactgtgactctctcttcaagcatgtgtctctgtaatgttcatgtctacaa 840
QY 867 CAAATATAGCAAGGCTCCATATGATGATACATGATGATGATGATGATGATGATGAT 926
DB 841 caaatatacaggaaggttccatagatgttatacctaacaattctcatccaacctgtact 900
QY 927 GGGAAACCTCTGAGATCTGTGTTTCATCTTTCGCTTCATATGCAAGTGCATCA 986
DB 901 gggaaacctgtgaagatctgtgttttcatcttcgccttcatatgccaagtgtcatca 960
QY 987 TTACGTGTGTATGAGCTGATGATCTTGGCTCAAGATGTCGCAATGCTCTGTGCT 1046
DB 961 ttacgtgtgtatgactgtatgtatctgtgcctcaagagtgctcagctgctccgtgct 1020
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DB 1021 ccaagaaagaaagaaagaaatcttcgaagatcacacagagatggtgtgtgtgtgtgt 1080
QY 1107 TGTTCATGCTGTGTGAGCTGCTCCATTCATATGATGATGATGATGATGATGATGAT 1166
DB 1081 tgttcattgtctgtgtgactccatccattcaatgcatcatataaagcctgtgttaca 1140
QY 1167 TCCAGAAACTAGCTTCCAGACTGTTTGTGCACTTGTGCTGCTGCTGCTGCTGCTG 1226
DB 1141 tccagaaactagcttccagactgttcttctgtcacttctgtcatgtcttgaagttaca 1200
QY 1227 ACAGTGTGCTACACGCTGCTTATGATGCTTGTGATGATGATGATGATGATGATGAT 1286
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DB 1381 aaatctggaagcgaagactgtccgttgccttaacagggctctatgccaattccgaacctt 1440
QY 1467 CACCAAGCTTAGAAGCACCACATGTATGTAAGCAGGTGCTTCAAGATGTGTAAGAG 1526
DB 1441 caccagcttagaagcaccatctgtatgtgaaagaggttgttcaagaatgtgtgaagga 1500
QY 1527 CTGTAATCTCTAGAAAGTCCCTTTTATGATCAACACTCTTCTCTGTGCGCA 1586
DB 1501 ctctaattctcttagaaagtgtcactatttagtcatccaacctcttctctctgtgcca 1560
QY 1587 CTCTGCTCTGCACTTAGAG 1607
DB 1561 ctctgctctgcaacttagaag 1581

RESULT 13
V61994
ID V61994 standard; cDNA: 2162 BP.
XX
AC V61994;

XX	11-JAN-1999	(first entry)
DT		
XX	Human mu-opioid receptor cDNA variant 10.	
DE		
XX	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;	
KW	predisposition; addiction; analgesic; anesthetic; anti-addictive;	
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;	
KW	cocaine; inherited alcoholism; human; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FH		
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FT	CDS	213..2040
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FT	misc-feature	855..856
FT		/*tag= c
FT		/note= "Site of intron 2"
FT	misc-feature	1376..1377
FT		/*tag= d
FT		/note= "Site of intron 3"
FT	mutation	1154
FT		/*tag= e
FT		/note= "Wild type G is replaced by A"
FN		
XX	W09833937-A2.	
PD		
XX	06-AUG-1998.	
XX		
PE	02-FEB-1998;	98WO-DE00382.
XX		
PR	03-FEB-1997;	97DE-1003925.
XX		
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PI		
PI	Hoehle M, Wendel B;	
XX		
DR	WPI: 1998-437487/37.	
PT		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -	
PT	used, e.g. to predict pre-disposition to addiction and for	
PT	development of analgesics, anaesthetics and anti-addiction agents	
XX		
PS	Claim 8; Page -: 26pp; German.	
XX		
XX	This sequence encodes a novel human mu-opioid receptor in which a G	
CC	nucleotide at position 1154 of the wild-type sequence represented in	
CC	V61984 is replaced by an A. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	cDNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anaesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism.	
CC	Note: This sequence is not represented in the specification and has	
CC	been constructed from the wild-type sequence represented in V61984 in	
CC	accordance with the specification.	
XX		
XX	Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other;	

Query Match	97.08;	Score 1561;	DB 19;	Length 2162;
Best Local Similarity	99.68;	Pred. No. 0;		
Matches 1575;	Conservative	0;	Mismatches 5;	Indels 1;
				Gaps 1.

OY	28	TGGAGGAGGCGCTATACCCAGAAGAAATGTCAgATCCTAAGTCGATCGATCCGCTTCCGCTTGA	87
Dd	1	tggaaaggaggtataacgaagaagaaatgtccaabttctaagcttgcgtcccttcgcactlga	60
OY	88	CGCnCTCTCTGTCTCAAGGCCAGGACTGGTTTCTGTAAAGAAACAGCAGAGCTGTGGCAGC	147
Dd	61	cgtcctctctctgtctcaagccaaagtgcgttttcgttaagaacaagcagggaccgtgtgcagc	120
OY	148	GCGGAAAAGAGCGGCTGAGGCGCTTGGAACCAGAACCTCTCGGTGCTCTGCGCTACTT	207
Dd	121	ggcgaaaggaagcgycgtgtagcgcttggaaccgcgaagtlctcgtgtccttgttacct	180
OY	208	CGCACAGC- GTGCCCCCGCCGCCGCTCATATACATGGACACAGACCGCTGGCCCCACAGAACG	266
Dd	181	cgcacagvgggtcccgcgccgcgcgtcaagtaccaitgaacagcagcgtctgcgcccaagaaog	240
OY	267	CCACAATTGCACGATGACCTTGGCGTACTCAAGTTGCTGCCACAGACCAGCCCCGGTT	326
Dd	241	ccagcaattgactgatgccttiggcgtlactcaagtgtcctcccaagacccccgcglt	300
OY	327	CCTGGGTCAATTGTCCCATTAGATGGCAACTGTGTCCAACCCATATGCGGTCCGAACCGCA	386
Dd	301	ctgtgttaaatctgtcccaattagatggaacactgtgcgaaccaatgcygttccgaacgcga	360
OY	387	CCGACCTGGGCGGAGAGAGACAGCCTGGCCCTCCGACCGGACAGTCCCTCATATGATCACGG	446
Dd	361	ccaacccgtgggcggaggaagaaagcctgtgccctccgcagcgcagctccctcatgatcaag	420
OY	447	CCATACGATCATGCGCCCTTACTCCATCGTGTGCGTGGGGGCTCTTGGAACACTTCC	505
Dd	421	ccatcacgatcatabgccctctactcatcagtgtgcgttggggctctcttgcgaaacctcc	480
OY	507	TGGTCATGTAATGTATGTTCAGATPACACCAAGATGAAGACTGCCACCAACTCTCATTT	566
Dd	481	tgtcgaqtaatgtaattgttcaagatacaaccaagvtgaagactgtccacaacatcatcaclt	540
OY	567	TCAAACCTTGCTCTGGCAGATGCCCTTAGCCACACAGTACCCCTGGCCCTCCAGAGTGTGAATT	626
Dd	541	tcaaacttgccttgcgcagatgcagtgcttagccaacagtaacctgtcccttcagagtgyaalt	600
OY	627	ACCTAATGGGAACATGGCCATTGGGAACCATCTTTGCAAGATAGTATCTTCATAGATT	686
Dd	601	acctaaatgggaacatggtccatltygaacacatcctlttgcaagtagtgaatcctacatagalt	660
OY	687	ACTTAACATATTACACAGATATTAACCCCTGCGACATGAAGTGTGATTCATCATGTG	746
Dd	661	actataacatfjttaacacagatatataccctctgcacacatgagtgttgaatgatacatlgt	720
OY	747	CAGTCTGCCACCTGTCAAGGCGCTTAGATTTCGGTACTGCCGAATGGCAAAATTATCA	806
Dd	721	cagltctgcacccctglaaagcctttagatttccgttatctcccgaaaatgcaaaatltacla	780
OY	807	ATGTCGTCAATGGATCTCTTTCAGCAATTGGATGGTTCCTTAATGTATAGGTATAA	866
Dd	781	atgtcgtcaaatggaatccctcttccacagcaatvgttccctcgttaaagtllcaatgagttcaaa	840
OY	867	CAAAATACAGGCAAGTTTCCATAGATTGTACATAACATTTCTCTCATCCAACTGGTACT	926
Dd	841	caaatcacagjcaaggtlcatatagattgttaacataacatctctcatccaacctgttact	900
OY	927	GGGAAAACCTCTGANAATATGTGTTTTATCTTGCCCTTCAATTATGGCAGTGCATCA	986
Dd	901	gggaaaaaccctgynaaaatctgttllcatatcttgccttcatltagccaggtccatca	960
OY	987	TTACCGTGTCTATNGACTATGATCTTGCGGCTCAAGAGTTCGCGCATGCTCTTGCT	1046
Dd	961	ttaccgtgtctatgascigtatgactcttgccctcaagagtgttcgcatgtcctcttgcct	1020
OY	1047	CCAAAAGAAAAAGACAGGAATCTTTCGAAGATACCAAGATGTGCTGCTGTGTGTGCTG	1106
Dd	1021	ccaaagaaaaagacaggaatccttcgaaggaatcaccaagatgtgtgtcgttgggtgtgtgt	1080

Qy	1047	CCAAAGAAAAGACAGGAATCTTCGAGGATCACCAGATGCTGCTGCTGCTG	1106
Db	1021	ccaaagaaaagacaggaatcttcgaagatcaccaagatgtgtcgtgtgtgtgtgctg	1080

QY	875	AGCAAGGTCATGATGATTTGACACTAACATTTCTCTATCCAACTGGTACTGGGAAAC	934
Db	849	aggcaaggctccatgatgatgtatacaataactctctcaacactggtaacttgggaaac	908
QY	935	CTGCAGAGATGTGTTTTCATCTTCGCGCTTCATTTATGCCAGTGCATCATTAACGGTG	994
Db	905	ctcgtaagatcttggtttcaactcttcgccttcaatatagccagtgctcaatttaacgtg	968
QY	995	TGCTATGACTGATGATCTTGCGCCTCAAGAGTGTCCGATGCTCTCTGAGCTCAAGAA	1054
Db	969	tgctatgactgatgatctcttgccctcaagggtgcgcgcatgctctctctgctccaagaa	1028
QY	1055	AAGGACAGGAATCTTTCGAAGATACACAGATGCTGCTGGTGGTGGTGGCTGTTCATC	1114
Db	1029	aaggacaggaaactcttcgaaggataccagagatggtcgtggtgtgtgtgtgtgtc	1088
QY	1115	GACTCTGGACTCCCATTCACATTCATTCATTCATTAAGGCTGGTATCAATCCAGAA	1174
Db	1089	gctctctggactcccatccaacttaactagtcataatgaagccttggtaaatccagaa	1148
QY	1175	ACTACGTTCCAGACTGTGTTCTTGGCACTTTCGATTTGCTTAGGTTACACAAACGCTGC	1234
Db	1149	actacgtccagactggtttcttcttggaacttcgcacttgcttagtgtaacaacagctgc	1208
QY	1235	CTCAACCCAGTCCCTTTATGACTTTTGATGATGAAAACTTCAACGATGCTTACAGAGCTTC	1294
Db	1209	ctcaaccagtcctcttatacgtcattcttgatgataaaacttcaacagatgcttcaagagcttc	1268
QY	1295	TGTATCCCAACTCTTCCCAACTTGAGCAACAAAACCTCAGTCGATTCGATTCGACAGACT	1354
Db	1269	tgtatcccaactctcttccaacatgtagaacaaaaacttcacttgaattcgtccagaacct	1328
QY	1335	AGAGACCAACCCGTCACGCGCCATACAGTGGATAGACTAATCATCAGCTGAAAAATCTG	1414
Db	1329	agaagaccacccctccacagcacaatacagtgatagaaactaatcatcagctagaanaactg	1388
QY	1415	GAAGCAGAAACTGCTCGCTTGCCCTTAACAGGTCATACGATTCAGCATCCGACCTTCACAAAGC	1474
Db	1389	gaagcagaagaactgctcgcttgcccttaacaaaggctccatgcacttcgccttccaaagc	1448
QY	1475	TTAGAAGCCACCATGTATGTGGAAACAGAGTGTCTCAAGATGTGTAGAGAGGCTCTAATT	1534
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QY	1535	CTCTAGGAAAGTGCCCTGCTTTTAGGTCAATCCAACTCTTCTCTCTGCGCATCTGCTC	1594
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QY	1595	TGCACATTAGAGG 1607	
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RESULT 15			
ID	288470		
XX	288470	standard; DNA; 2162 BP.	
XX	AC	288470:	
XX	DT	11-MAY-2000 (first entry)	
XX	DE	Human mu opioid receptor gene.	
XX	DE		
KW		Human; mu opioid receptor; hMOR1; diagnosis; addiction; constipation;	
KW		diarrhoea; decreased immune response; stress; gastrointestinal motility;	
KW		immune response; hypothalamus pituitary adrenal axis; gonadal axis;	
KW		pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;	
KW		antioxytic; alcohol; ds.	
XX		Homo sapiens.	
XX			
PN	WO200003024-A2.		

[illegible]

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 19:12:11 : Search time 838.13 Seconds
(without alignments)
11876.819 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGAGCCTCTGTGACT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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C 2	332.2	20.1	1053	114	CNS04AC3T	AL128994_Tetradomor
C 3	227	14.1	525	102	AQ767579	AQ767579_HS_3206L
4	213.8	13.3	876	113	CNS02261	AL177778_Tetradomor
5	211	13.1	877	113	CNS02SC2	AL1211691_Tetradomor
C 6	191	11.9	842	113	CNS025KUC	AL121007_Tetradomor
C 7	186.8	11.6	710	113	CNS01ZMG	AL174481_Tetradomor
C 8	184.2	11.4	433	22	AM489031	AM489031_Ui-M-BH3-
C 9	158.6	9.9	927	114	CNS04RP2	AL1304175_Tetradomor
C 10	158.2	9.8	881	114	CNS03JUCN	AL246704_Tetradomor
C 11	155.4	9.7	424	21	AM373832	AM373832_QV3-BT053
C 12	137.6	8.5	457	19	AM047705	AM047705_Ui-M-BH1-
C 13	136.4	8.1	245	98	AQ488720	AQ488720_RPCT1-11-2
C 14	130.4	8.5	642	34	BE253309	BE253309_601114162
15	124	7.7	546	109	AZ226406	AZ226406_RPCT-23-8
16	123.8	7.7	937	114	CNS03GSG	AL243485_Tetradomor
C 17	117.2	7.3	995	114	CNS04ROB	AL304223_Tetradomor
C 18	115.4	7.2	183	39	R81583	R81583_Y04D04.r1
19	112.2	7.0	638	25	AM919332	AM919332_EST350636
20	108	6.7	656	14	AL119185	AL119185_DK2P761N
C 21	107.2	6.7	534	23	AM652898	AM652898_101337
C 22	98.2	6.1	794	113	CNS01WC1	AL170218_Tetradomor
C 23	92.6	5.8	992	113	CNS022ZG	AL121605_Tetradomor
C 24	90.8	5.6	844	113	CNS03CLX	AL237966_Tetradomor
25	89	5.5	951	38	R31964	R31964_Y062C10.r1
C 26	80.4	5.0	103	112	CNS01SK5	AL165326_Tetradomor
27	79	4.9	1029	114	CNS03SOZ	AL158812_Tetradomor
28	72.4	4.5	552	14	AJ393659	AJ393659_AJ393659
29	71.2	4.4	640	34	BE198338	BE198338_uf77d12.Y
30	70.8	4.4	543	22	AM516933	AM516933_xc04a06.x
C 31	70	4.3	817	114	CNS03DLV	AL1239260_Tetradomor
32	69	4.3	378	114	CNS03HDA	AL244747_Tetradomor
33	68.8	4.3	557	23	AM669715	AM669715_113242.MA
34	68.4	4.2	595	7	AA940565	AA940565_vz46e06.r
35	68.2	4.2	1002	113	CNS02CZB	AL191792_Tetradomor
36	66.8	4.1	529	23	AM653917	AM653917_102840.MA
37	66.6	4.1	486	23	BE128304	BE128304_DEPA2054
C 38	66.2	4.1	485	22	AM435011	AM435011_Ui-H-BW1-
C 39	66.2	4.1	530	19	AM028270	AM028270_wv68b03.x
C 40	66.2	4.1	738	10	A1475600	A1475600_tc92h03.Y
41	65.8	4.1	592	14	AL046512	AL046512_DK2P586M
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43	65.4	4.1	391	38	N93987	N93987_z666d09.r1
44	65.4	4.1	932	113	CNS02STR	AL1621932_Tetradomor
C 45	64.2	4.0	434	9	AI263329	AI263329_q120C06.x

RESULT 1
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LOCUS	B82759	520 bp	DNA	GSS	09-APR-1999
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ACCESSION	DNA sequence.				
VERSION	B82759				
KEYWORDS	B82759.1	GI:2869782			
SOURCE	GSS.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 520)				
JOURNAL	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Shh,E., Wible,C., de Jong,P. and				
COMMENT	Venter,J.C.				
	Use of BAC End Sequences for Sequence-Ready Map Building (1998)				
	Unpublished (1998)				
	Other_GSS: RPc11-17K22.TVB				

Location/Qualifiers
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/clone_1b="RPC1-11"
/sex="Male"
/cell_type="lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI
RPC11 Human Male BAC Library"
BASE COUNT      101 a      153 g      112 t
ORIGIN

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Best Local Similarity	97.1%;	Pred. No. 3.2e-85;		
Matches 340: Conservative	0;	Mismatches 9;	Indels 1;	Gaps

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Db	520	CGGTCTCTCTGGTAACTCCGACAGCGGTGCCCGCCGACGTAGTACATGGACAGCA	465
Oy	249	GGCGTCCGCCCCAGCAAGCCAGCAATTGCACTGATGCTTGGCTTACTCAAGTTGCTCC	305
Db	460	GGCGTGCACCAACGAGACGCCAGCAATTGCACTGATGCTTGGCTTACTCAAGTTGCTCC	401
Oy	309	CAGCACCCAGCCCGGGTTCTCTGGGTCAACTGTCTCCACTTATGATGGCAACTGTGCCAGC	365
Db	400	CAGCACCCAGGAGAGGGTCTCTGGGTCAACTGTCTCCACTTATGATGGCAACTGTGCCAGC	341
Oy	369	CATGGAGTCCGACACCGCACCGACCTGGGCGGGAGAGAGACGCTGTGCCCTCCGACCGCA	428
Db	340	CATGGAGTCCGACACCGCACCGACCTGGGCGGGAGAGAGACGCTGTGCCCTCCGACCGCA	283
Oy	429	GTCCCTTCATGATCAGCGGCATCAGATCATGGCCCTCTACTCCATCGTGTGGTGTGG	488
Db	280	GTCCCTTCATGATCAGCGGCATCAGATCATGGCCCTCTACTCCATCGTGTGGTGTGG	221
Oy	489	GGCTTTTGGGAACTTCTCTGGTCAATGTATGTGATTTGTCAGATACCAACAG	538

JOURNAL REFERENCE	JOURNAL TITLE	JOURNAL REFERENCE	JOURNAL TITLE	JOURNAL REFERENCE	JOURNAL TITLE
freshwater pufferfish Tetraodon nigroviridis	Unpublished	freshwater pufferfish Tetraodon nigroviridis	Unpublished	freshwater pufferfish Tetraodon nigroviridis	Unpublished
2 (bases 1 to 877)	2 (bases 1 to 877)	2 (bases 1 to 877)	2 (bases 1 to 877)	2 (bases 1 to 877)	2 (bases 1 to 877)
Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.	Roset-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fizam,C., Mincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Unpublished	Unpublished	Unpublished	Unpublished	Unpublished	Unpublished
3 (bases 1 to 877)	3 (bases 1 to 877)	3 (bases 1 to 877)	3 (bases 1 to 877)	3 (bases 1 to 877)	3 (bases 1 to 877)
Genoscope.	Genoscope.	Genoscope.	Genoscope.	Genoscope.	Genoscope.
Direct Submission	Direct Submission	Direct Submission	Direct Submission	Direct Submission	Direct Submission
Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon .
Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers
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/clone="151H06"	/clone="151H06"	/clone="151H06"	/clone="151H06"	/clone="151H06"	/clone="151H06"
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/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"	/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"	/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"	/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"	/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"	/note="Genoscope sequence ID : C0AG161DD03SP1-end : PUC-Orl"
BASE COUNT	201 a 249 c 214 g 197 t 16 others	BASE COUNT	201 a 249 c 214 g 197 t 16 others	BASE COUNT	201 a 249 c 214 g 197 t 16 others
ORIGIN		ORIGIN		ORIGIN	
Query Match	13.1%; Score 211; DB 113; Length 877;	Query Match	13.1%; Score 211; DB 113; Length 877;	Query Match	13.1%; Score 211; DB 113; Length 877;
Best Local Similarity	74.2%; Pred. No. 1.4e-51;	Best Local Similarity	74.2%; Pred. No. 1.4e-51;	Best Local Similarity	74.2%; Pred. No. 1.4e-51;
Matches	262; Conservative 3; Mismatches 88; Indels 0; Gaps 0;	Matches	262; Conservative 3; Mismatches 88; Indels 0; Gaps 0;	Matches	262; Conservative 3; Mismatches 88; Indels 0; Gaps 0;
OY	527 AGATACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	527 AGATACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	527 AGATACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
DB	348 AGGTACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	348 AGGTACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	348 AGGTACACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
OY	587 GCCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	587 GCCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	587 GCCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
DB	408 GCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	408 GCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	408 GCTTAGCCACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
OY	647 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	647 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	647 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
DB	468 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	468 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	468 TTTCGACCAATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
OY	707 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	707 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	OY	707 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
DB	528 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	528 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT	DB	528 ATATCAGCCATGATAGAGATGCGACCAACATCTTCATTTACCTGTGCTGCGAGAT
OY	767 GCCTTAGCCATGATAGAGATGCGACCAACATCT				

[illegible]

TITLE Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 881)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetradon>.

FEATURES
source
1. 881
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="031C21"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG031AB1LP1-end : T7"

BASE COUNT 202 a 212 c 236 g 231 t

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Best Local Similarity 76.4%; Pred. No. 7.4e-36;
Matches 207; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

525 TCAGATACCAAGATAGACAGCTGCGACCAACATCTACATTTGACCTGCTGGCAG 584
|||||
270 TTAGTACCAACAAATAGACGCGCACAAACATCTACATTTGACCTGCTGGCAG 211
|||||
585 ATGCTAGGACCAAGATAGACCTGCTGCGACAGTGTGAATTAATGGAACATGCG 644
|||||
210 ACGGCTGTCACAGACAGCGCTTCCCTTCAGAGCGTCACTACCTGATGGCGACG 151
|||||
645 CATTTGACCAATCTTTGCAAGATAGTATCTCATAGATTAATTAACATGTTACCA 704
|||||
150 C-TTCGGCGAGCTGCTGCGAAGATCTCATGCTCATGACTACCAACATGTTCACT 92
|||||
705 GCATATCACACCTCTGACCATGATGTGATGATCATGATGAGTGGCACCCTGCA 764
|||||
91 CCACTTACAGCTTACCAACATGAGCGTGGACGCTGAGCGGTGTGCTGCTGCTGCA 32
|||||
765 AGGCTTGAATTTCCGCTACTCCCGGAATGC 795
|||||
31 AAGGCTGAGCTTCAAGACGCGGCAACGC 1

RESULT 11
AM373832
LOCUS AM373832 654 bp mRNA EST 04-FEB-2000
DEFINITION QV3-BT0537-221299-048-h10 BT0537 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM373832
VERSION AM373832.1 GI:6878486
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 654)
HCGP <http://www.ludwig.org.br/OESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV3&t2-QV3-BT0537->

221299-048-h10&t3=1999-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 639.
Location/Qualifiers
1. 654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="BT0537"
/dev_stage="Adult"
/note="Organ: Breast; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 117 a 210 c 185 g 142 t

ORIGIN

Query Match 9.7%; Score 155.4; DB 21; Length 654;
Best Local Similarity 68.9%; Pred. No. 4.5e-35;
Matches 213; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

450 TCAGATCATGACGCTCTACTCCATGCTGCGTGGGAGGCTTCGGAACCTTCCTGG 509
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346 TCACATCATGTCGGGCTCTACTCCGCTGTGTGTGAGGAGGCTCTGGGAATGCTCTG 405
|||||
510 TCATGATGATGATGTCAGATACCAAGATGAAGACTGCGACCAACATCTACATTTCA 569
|||||
406 TCATGATGATGATGATGTCAGATACCAAGATGAAGACTGCGACCAACATCTACATTTCA 465
|||||
570 ACCTTGTCTGCGAGATGCTTACGACCAAGTACCTGCTGCTGCTGCTGCTGCTGCTG 629
|||||
466 ACCTGCGCTGCGGACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525
|||||
630 TAATGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689
|||||
526 TCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
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690 ATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
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586 ACAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
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750 TCTGCGACG 758
|||||
646 TCTGCGACG 654

RESULT 12
AM047705/c
LOCUS AM047705/c 427 bp mRNA EST 18-SEP-1999
DEFINITION UI-M-BH1-a10-f-04-0-UI-s1 NIH-BMAP-M-S2 Mus musculus cDNA clone
UI-M-BH1-a10-f-04-0-UI 3', mRNA sequence.
ACCESSION AM047705
VERSION AM047705.1 GI:5908234
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 427)
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
CONTACT: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706

ACCESSION	BE252309
VERSION	BE252309.1 GI:9122447
KEYWORDS	E8T.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 642)
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) Cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC library.
FEATURES	location/qualifiers 1..642 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_1 IMAGE:3354783 /clone_1 ID="NIH_MGC_16" /tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pORF7; Site: J; XhoI; Site: 2; EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
BASE COUNT	136 a 179 c 159 g 168 t
ORIGIN	
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Best Local Similarity	53.0%; Pred. No. 1,3e-27;
Matches 303; Conservative	0; Mismatches 266; Indels 3; Gaps
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Db	50 TCACATTCATCATTTTGTGTGCTGCCATCATTTGTTGTGTGGCAACACTTGTCAATT 109
OY	516 ATNGATTTGTCSAATNACCAGAANGAACTGTGCACCAATCATATTTCACACTTG 575
Db	110 AATGATCTCTCCGGCATCCCAAGAGAAAGAACCATCACCAATTTTACATCTCAACTGG 169
OY	576 CTCTGGCAGATGACTTTAGCCACACAGTACCCCTCCCTCCAGTAGTGTAATTACCTATGG 635
Db	170 CCATGCAGATGAGACTTTCATGCTGGGTGTGCGCTTTCTTGATGAGAGTGCGCTGG 229
OY	636 GAACATGGCCATTGGGAACCATCTTTTSCAAGATAGTATCTCCATAGATTATCATATAACA 695
Db	230 TCCACTGCCCCCTTGGCAGAGCCATTTTCCGGGTGTCATACGTGTGATGGCAATCATATC 289
OY	696 TGATCACCAGATATATCACTCTGACACAGATAGTGTGATCGATATTCATTCATCTGGCC 755
Db	290 AGTTCCACGATATCTTCTGCTGACAGTCATAGACATGACCATTAATCTGCTGTGCTGC 349
OY	756 ACCCTGTCAAGGCTTAGATTTCGTACTCCCAGAAATGCGAAAATATATCATGTGTGCA 815
Db	350 ACCCATCAATCTGGCCCAAGTGAAGAACCCCGGACGGCCAAAGATGATACCATATGCTGG 409
OY	816 ACTGATCTCTCTTTCACACCAATGTGCTTTCGTGTAATGTATCATGGCT---ACAACAAT 872
Db	410 TTGTGGGAGATCTCTGCTGTGATCATTTGCCCATCATATATATATATGTGGGCTCCGAGCA 469

Qy	873	ACAGCAGAGTTCATAGATATGTGTACACTAACATATCTGCATCCAACTGGATCGGGGAA	932
Db	470	ACCAATGGGGGAGAAAGCAGCTGCACACATCACTGTGCCAGGTGATCTTGGGCTTGTA	529
Qy	933	ACCTGCTGAATATCTGTGTTTTCATCTTTCGCTTCATTTATTCAGAGTGTCTATTA	992
Db	530	CAGGTTTCATATCATCACTACATCTTTCGCGGTTCTGTGTACCCCTCACCATCATCTG	589
Qy	993	TGTGCTATGACATGATATCTTGGCCCTCAG	1024
Db	590	TTTGCTACCTGTTTCATTTATTCATCAAGGTGAAG	621
RESULT	15		
LOCUS	AZ226406	546 bp	DNA
DEFINITION	RPci-23-80H6.TJ RPci-23	Mus musculus genomic clone RPci-23-80H6,	
ACCESSION	AZ226406		
VERSION	AZ226406.1	GI:8534455	
KEYWORDS	SSS		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 546)		
TITLE	Zhao S., Nieman, W., Feldblum, T., Malek, J., Shatsman, S., Akirret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, T., and Fraser, C.M.		
JOURNAL	Mouse BAC End Sequences from Library RPci-23		
COMMENT	Unpublished (1999)		
	other GSSs: RPci-23-80H6.TJ		
	Contact: Shaying Zhao		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: szhao@tigr.org		
	Clones are derived from the mouse BAC library RPci-23. For BAC library availability, please contact Pieter de Jong (pieter@edj.org.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (http://www.reschgenetics.com). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html		
	Plate: 80 row: H column: 6		
	Seq primer: SP6		
	Class: BAC ends.		
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	/strain="C57BL/6J"		
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	/clone="RPci-23-80H6"		
	/clone_id="RPci-23"		
	/sex="Female"		
	/lab_host="DH10B"		
	/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site:1; EcoRI, Site:2; EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."		
BASE COUNT	169 a	102 c	110 g
ORIGIN	165 t		
Query Match	7.7%	Score 124;	DB 109; Length 546;
Best Local Similarity	68.3%	Pred. No. 9,5e-26;	
Matches 172;	Conservative	0; Mismatches 80;	Indels 0; Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 21:43:02 ; Search time 1824.62 Seconds

(without alignments)
3853.845 Million cell updates/sec

Title: us-08-305-518-7

Perfect score: 1610
Sequence: 1 CCGATGAGCCTGTGACT.....GCTCTGACATTAGAGCCG 1610

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1033670 seqs, 2183789903 residues

Word size : 35

Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
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12: gb_ro:*
13: gb_sy:*
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15: em_fun:*
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81: gb_pi14:*
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83: gb_pi16:*
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89: gb_pi22:*
90: gb_pi23:*
91: gb_pi1:*
92: gb_pi2:*
93: gb_pi1:*
94: gb_pi2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1610	100.0	1610	67	HUMOPTIOIDA
2	1236	78.0	2162	5	A87781
3	1240	77.0	2162	67	HUMWOB1X
4	1086	67.5	1473	66	HSU12569
5	523	32.5	124569	88	AL359850
6	523	32.5	131426	85	AL136444
7	487	30.2	1598	66	HSOPRMT2
8	406	25.2	124569	88	AL359850
9	406	25.2	182048	80	AC021743
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15	209	13.0	98104	66	HSJ04402L9
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17	141	9.23	293	91	AF100548
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22	74	4.6	77313	76	AC022855
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25	59	3.7	1334	12	AF074973
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27	59	3.7	1543	12	AF074974
28	59	3.7	1610	12	MMT26915
29	59	3.7	1729	12	AF167568
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40	47	2.9	2397	12	RATRORB
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					L36645 Sus scrofa
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					U76915 Mus musculu
					AF167568 Mus musculu
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					AC055776 Mus musculu
					AF266480 Ovis arie
					AC022855 Homo sapi
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					I22455 Ratt mu opio
					U02083 Rattus norv
					L13069 Rattus norv
					L10664 Rattus norv
					U16349 Rat mRNA fcd
					S77863 mu-opioid r
					U67928 Cavia porcea
					S79903 mu opiod r

ALIGNMENTS

RESULT	1			
HUMOPIOIDA				
LOCUS				
DEFINITION	HOMOPIOIDA	1610 bp	mRNA	
ACCESSION	Homo sapiens opioid receptor mRNA, complete cds.			03-AUG-1995
VERSION	L29301			
KEYWORDS	L29301.1 GI:459831			
SOURCE	opioid receptor.			
ORGANISM	Homo sapiens.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 1610)			
JOURNAL	Mester,A., Hurley,J.H., Bye,L.S., Campbell,A.D., Chen,Y., Tian,M., Liu,J., Schuman,H. and Yu,L.			
MEDLINE	The human mu opioid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C			
FEATURES	J. Neurosci. 15 (3), 2396-2406 (1995)			
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OY	181	GAAAGTCTGCTGCTCTGCTACTCTGACACGTGCCCCGGCGCGCTTACATACAT	240		
Db	181	GAAAGTCTGCTGCTCTGCTACTCTGACACGTGCCCCGGCGCGCTTACATACAT	240		
OY	241	GGACAGCAGCGCTGCCCCCGCCAGAACGCCAGCAATGTGCACTATGCTTGGGGTACTCAAG	300		
Db	241	GGACAGCAGCGCTGCCCCCGCCAGAACGCCAGCAATGTGCACTATGCTTGGGGTACTCAAG	300		
OY	301	TTGCTCCCGAGACCCAGCCCGGTTCTGTGGGTCACTTGTCCACTTATAGATGGCAACT	360		
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OY	361	GTCCGACCCATGCGGCTCCGAGACCCGACCTGCGGGGAGAACAGCCGTGTCCTCC	420		
Db	361	GTCCGACCCATGCGGCTCCGAGACCCGACCTGCGGGGAGAACAGCCGTGTCCTCC	420		
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OY	481	CGTGGTGGGGCTCTTCGGAACCTTCTGTGTCATGTATGTGTGACATACACCAAGAT	540		
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Db	661	TTGCAAGATAGTGAATCTCCATAGATTACTATTAACATGTTCACCGCATATTACACCTGTG	720		
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Db	721	CACCATGAGTGTATGATGATACATTTGCAAGTCTGCCACCTGTCAAGGCTTAGATTTCCG	780		
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Db	781	TATCCGCCGGAATGCCAAATATTAATCAATATGTCGAACTGGATCTCTTCCAGCATTTGG	840		
OY	841	TCTCTCTATATGTTTCATGGCTACACAAATATACAGCAAGTTCCATAGATTGTACACT	900		
Db	841	TCTCTCTATATGTTTCATGGCTACACAAATATACAGCAAGTTCCATAGATTGTACACT	900		
OY	901	AACATCTCTATCAACCTGTGTAAGTGGAAACCTGTGAAGATCTGTGTTTCATCTT	960		

Db 901 AACATTCCTCATCCACCTGGTACTGGGAAACCTGCTGAGATCTGTGTTTCATCT 960
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RESULT 2
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LOCUS A87781
DEFINITION Sequence 7 from Patent WO9833937.
ACCESSION A87781
VERSION A87781.1 GI:6736383
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2162)
AUTHORS Hoehe, M. and Wendel, B.
TITLE GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE
VARIANTS, POLYMORPHISMS AND MUTATIONS THEREOF
JOURNAL Patent: WO 9833937-A 06-AUG-1998;
HOEHE MARGRET (DE); WENDEL BIRGIT (DE)
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BASE COUNT 562 a 565 c 458 g 575 t 2 others
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Query Match 78.0%; Score 1256; DB 5; Length 2162;
Best Local Similarity 99.7%; Pred. No. 0;

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QY 88 CGCT 147
Db 61 CGCT 120
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QY 387 CCGAGCTGGGGGGGAG 446
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RESULT 3
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LOCUS HUMMORIX 2162 bp mRNA PRI 08-AUG-1994
DEFINITION Human mu opiate receptor (MOR1) mRNA, complete cds.
ACCESSION L25119
VERSION L25119.1 GI:452072
KEYWORDS Mu opiate receptor.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A.
and Uhl,G.R.
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 94139928
FEATURES
SOURCE location/Qualifiers
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BASE COUNT 563 a 566 c 455 g 576 t 2 others
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Best Local Similarity 99.78; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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REFERENCE	3 (bases 1 to 1473)
AUTHORS	Bare, L.A.
TITLE	Direct Submission
JOURNAL	Submitted (24-JUL-1994) Lance A. Bare, Ohmeda, PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA
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1 GCAGAGAGAAATGTCAGATGCTCAGCTGAGTCCCTCGCTGACGCTCTCTGTCTC	60
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61 AGCCAGAGCTGGTTTCTGTAAAGAAACAGCAGAGCTGTGCGAGCGCGAAAGAGCGGC	120

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 Db 121 TGAGGCGCTTGGAAACCCGAAAAGTCTCGGTGCTCTGGCTACCTGACAGCAGCGTGCCCG 180
 QY 223 CCGGCGCTGAGTACATGAGCAGCAGCGTGCCTCCCAAGAACGCGCAGCAATTCATGA 282
 Db 181 CCGGCGCTGAGTACATGAGCAGCAGCGTGCCTCCCAAGAACGCGCAGCAATTCATGA 240
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 QY 343 CCACCTAGATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 402
 Db 301 CCACCTAGATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 360
 QY 403 AGACAGCGCTGAGTACATGAGCAGCAGCGTGCCTCCCAAGAACGCGCAGCAATTCATGA 462
 Db 361 AGACAGCGCTGAGTACATGAGCAGCAGCGTGCCTCCCAAGAACGCGCAGCAATTCATGA 420
 QY 463 CCTCTACCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 522
 Db 421 CCTCTACCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 480
 QY 523 TGTGAGATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 582
 Db 481 TGTGAGATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 540
 QY 583 AGATGCGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 642
 Db 541 AGATGCGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 600
 QY 643 GCCATTGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 702
 Db 601 GCCATTGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 660
 QY 703 CAGCATATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 762
 Db 661 CAGCATATGAGCAACCTGCTCGGACCGCATGCGGATCGCAACGCGCAGCGTGCCTCC 720
 QY 763 CAGGCGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 822
 Db 721 CAGGCGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 780
 QY 823 CCTCTACCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 882
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 QY 883 TTCCATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 942
 Db 841 TTCCATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 900
 QY 943 GATCTGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1002
 Db 901 GATCTGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 960
 QY 1003 ACTGATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1062
 Db 961 ACTGATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1020
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 Db 1021 GAATCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1080
 QY 1123 GATCTGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1182
 Db 1081 GATCTGCTGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1140
 QY 1183 CCAGATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1242
 Db 1141 CCAGATGAGTACATGAGTCTCCCAAGAACGCGCAGCGTGCCTCCCAAGAAC 1200

QY 1243 AGCTCTTATGATCTTGCATGAGTAACTTCAAGCATGCTTACAGAGTCTGATCCC 1302
 Db 1201 AGCTCTTATGATCTTGCATGAGTAACTTCAAGCATGCTTACAGAGTCTGATCCC 1260
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 Db 1261 AACCTCTTCAACATTTGAGCAACAAACTCCATCGAATTCGTGAGAACTAGAGACCA 1320
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 Db 1321 CCCCTCCAGCGCAATGAGTACAGTAACTAATCATCAG 1360

RESULT 5
 AL359850
 LOCUS
 DEFINITION
 Homo sapiens chromosome 6 clone RP11-157M8, *** SEQUENCING IN
 PROGRESS.***, 40 unordered pieces.
 ACCESSION
 AL359850.2 GI:9367619
 VERSION
 HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 124569)
 Sins., S.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Direct Submission
 Submitted (15-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Jul 22, 2000 this sequence version replaced gi:8977775.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: BA157M8
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 102271 bases at least Q40
 Consensus quality: 110329 bases at least Q30
 Consensus quality: 115261 bases at least Q20
 Insert size: 12068; sum-of-contigs
 Quality coverage: 145960; agarose-1p
 Quality coverage: 3.24x in Q20 bases; sum-of-contigs quality
 coverage: 2.68x in Q20 bases; agarose-1p

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 40 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1459: contig of 1459 bp in length
 1460 1559: gap of 100 bp
 1560 3320: contig of 1761 bp in length
 3321 3420: gap of 100 bp
 3421 5562: contig of 2142 bp in length
 5563 5662: gap of 100 bp
 5663 9774: contig of 4112 bp in length
 9775 9874: gap of 100 bp
 9875 11521: contig of 1647 bp in length
 11522 11621: gap of 100 bp
 11622 14784: contig of 3163 bp in length
 14785 14884: gap of 100 bp
 14885 16929: contig of 2045 bp in length
 16930 17029: gap of 100 bp

* 17030 21195: contig of 4166 bp in length
* 21196 21295: gap of 100 bp
* 21296 22547: contig of 1252 bp in length
* 22548 22647: gap of 100 bp
* 22648 28063: contig of 5416 bp in length
* 28064 28163: gap of 100 bp
* 28164 30406: contig of 2243 bp in length
* 30407 30506: gap of 100 bp
* 30507 32053: contig of 1547 bp in length
* 32054 32153: gap of 100 bp
* 32154 34236: contig of 2083 bp in length
* 34237 34336: gap of 100 bp
* 34337 36558: contig of 2222 bp in length
* 36559 36658: gap of 100 bp
* 36659 38408: contig of 1750 bp in length
* 38409 38508: gap of 100 bp
* 38509 40660: contig of 2152 bp in length
* 40661 40760: gap of 100 bp
* 40761 42115: contig of 1355 bp in length
* 42116 42215: gap of 100 bp
* 42216 45404: contig of 3189 bp in length
* 45405 45504: gap of 100 bp
* 45505 47767: contig of 2263 bp in length
* 47768 47867: gap of 100 bp
* 47868 50333: contig of 2466 bp in length
* 50334 50433: gap of 100 bp
* 50434 53910: contig of 3477 bp in length
* 53911 54010: gap of 100 bp
* 54011 55124: contig of 1114 bp in length
* 55125 55224: gap of 100 bp
* 55225 57215: contig of 1991 bp in length
* 57216 57315: gap of 100 bp
* 57316 58382: contig of 1067 bp in length
* 58383 58482: gap of 100 bp
* 58483 80755: contig of 22273 bp in length
* 80756 80855: gap of 100 bp
* 80856 81866: contig of 1011 bp in length
* 81867 81966: gap of 100 bp
* 81967 85210: contig of 3244 bp in length
* 85211 85310: gap of 100 bp
* 85311 87074: contig of 1764 bp in length
* 87075 87174: gap of 100 bp
* 87175 91511: contig of 4337 bp in length
* 91512 91611: gap of 100 bp
* 91612 92650: contig of 1039 bp in length
* 92651 92750: gap of 100 bp
* 92751 95618: contig of 2868 bp in length
* 95619 95718: gap of 100 bp
* 95719 97558: contig of 1840 bp in length
* 97559 97658: gap of 100 bp
* 97659 100174: contig of 2516 bp in length
* 100175 100274: gap of 100 bp
* 100275 101789: contig of 1515 bp in length
* 101790 101889: gap of 100 bp
* 101890 103053: contig of 1164 bp in length
* 103054 103153: gap of 100 bp
* 103154 106517: contig of 3364 bp in length
* 106518 106617: gap of 100 bp
* 106618 107662: contig of 1045 bp in length
* 107663 107762: gap of 100 bp
* 107763 110688: contig of 2926 bp in length
* 110689 110788: gap of 100 bp
* 110789 115340: contig of 4552 bp in length
* 115341 115440: gap of 100 bp
* 115441 124569: contig of 9129 bp in length.
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/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-157M8"
/clone_1lb="RPc1-11.1"
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fragment_chain:1"
3421. .5562
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5663. .9774
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9875. .11521
/note="assembly_fragment:00015
fragment_chain:2"
11622. .14784
/note="assembly_fragment:01088
fragment_chain:2"
14885. .16929
/note="assembly_fragment:01190
fragment_chain:2"
17030. .21195
/note="assembly_fragment:00007
fragment_chain:3"
21296. .22547
/note="assembly_fragment:00142
fragment_chain:3"
22648. .28063
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28164. .30406
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fragment_chain:5"
34337. .36558
/note="assembly_fragment:00743
fragment_chain:6"
36659. .38408
/note="assembly_fragment:00187
fragment_chain:6"
38509. .40660
/note="assembly_fragment:00749
fragment_chain:7"
40761. .42115
/note="assembly_fragment:00794
fragment_chain:7"
42216. .45404
/note="assembly_fragment:01106
fragment_chain:8"
45505. .47767
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fragment_chain:8"
47868. .50333
/note="assembly_fragment:00023"
50434. .53910
/note="assembly_fragment:00085"
54011. .55124
/note="assembly_fragment:00099"
55225. .57215
/note="assembly_fragment:00139"
57316. .58382
/note="assembly_fragment:00161"
58483. .80755
/note="assembly_fragment:00266"
80856. .81866

misc_feature

Query Match 32.5%; Score 523; DB 88; Length 124569;
Best Local Similarity 100.0%; Pred. No. 3e-287;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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QY 880 AGGTTCCATGATGTTAGACTAATCTCTCATCCCAACCTGGAGGAAAACCTGCT 939
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Db 54492 AGGTTCCATGATGTTAGACTAATCTCTCATCCCAACCTGGAGGAAAACCTGCT 54551
QY 940 GAAGATCTGTGTTTATCTTCCCTTCATTATGCAAGTGCATCATACCGTGTGCTA 999
    |||||||
Db 54552 GAAGATCTGTGTTTATCTTCCCTTCATTATGCAAGTGCATCATACCGTGTGCTA 54611
QY 1000 TGACATGATGATTTGGCGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAAGGA 1059
    |||||||
Db 54612 TGACATGATGATTTGGCGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAAGGA 54671
QY 1060 CAGGATCTTCGAAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
    |||||||
Db 54672 CAGGATCTTCGAAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 54731
QY 1120 CTGGACTCCCATTCACATTTACATCATTAAGCCTTGTTACATCCAGAACTAC 1179
    |||||||
Db 54732 CTGGACTCCCATTCACATTTACATCATTAAGCCTTGTTACATCCAGAACTAC 54791
QY 1180 GTTCCAGACTGTTTCTTGGGACTTCTGATGCTTATAGTTACAAACAGCTGCTCAA 1239
    |||||||
Db 54792 GTTCCAGACTGTTTCTTGGGACTTCTGATGCTTATAGTTACAAACAGCTGCTCAA 54851
QY 1240 CCCAGTCTTTATGATCTGATGAAACCTCAACAGATGCTGAGAGTCTGTAT 1299
    |||||||
Db 54852 CCCAGTCTTTATGATCTGATGAAACCTCAACAGATGCTGAGAGTCTGTAT 54911
QY 1300 CCCAACCTTCTTCCACATTTGAGCAACAAACCTCCACTCGAATTCGTAGAACTAGAGA 1359
    |||||||
Db 54912 CCCAACCTTCTTCCACATTTGAGCAACAAACCTCCACTCGAATTCGTAGAACTAGAGA 54971
QY 1360 CCACCCCTCCAGGCGCAATTCAGTGTAGTAAGTAATATCATCAG 1402
    |||||||
Db 54972 CCACCCCTCCAGGCGCAATTCAGTGTAGTAAGTAATATCATCAG 55014

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RESULT 6
AL136444/c DNA HTG 23-JUL-2000
LOCUS AL136444.1 131426 bp
DEFINITION Homo sapiens chromosome 6 clone RP3-366F13, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
ACCESSION AL136444
VERSION AL136444.11 GI:9437221
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 131426)
Direct Submission
Submitted (22-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 24, 2000 this sequence version replaced gi:9368896.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj366f13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 130583 bases at least Q40
Consensus quality: 131107 bases at least Q30
Consensus quality: 131274 bases at least Q20
Insert size: 140334; sum-of-ctrls
Insert size: 140334; 3.3% error; agarose-1p

```

Quality coverage: 0.00x in Q20 bases; sum-of-ctrls Quality coverage: 0.00x in Q20 bases; agarose-1p

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.

FEATURES

1..130047: contig of 130047 bp in length
 * 130048 130147: gap of 100 bp
 * 130148 131426: contig of 1279 bp in length.
 Location/Qualifiers
 1..131426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP3-366F13"
 /clone_1bp="RP3-3"

misc.feature

1..130047
 /note="assembly-fragment:00526.0"

misc.feature

130148..131426
 /note="assembly-fragment:00799.0"

BASE COUNT

40768 a 24297 c 24755 g 41506 t 100 others

ORIGIN

Query Match

32.5%; Score 523; DB 85; Length 131426;
 Best Local Similarity 100.0%; Pred. No. 3e-187;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 880 AGGTTCCATGATGTTAGACTAATCTCTCATCCCAACCTGGAGGAAAACCTGCT 939
    |||||||
Db 45747 AGGTTCCATGATGTTAGACTAATCTCTCATCCCAACCTGGAGGAAAACCTGCT 45688
QY 940 GAAGATCTGTGTTTATCTTCCCTTCATTATGCAAGTGCATCATACCGTGTGCTA 999
    |||||||
Db 45687 GAAGATCTGTGTTTATCTTCCCTTCATTATGCAAGTGCATCATACCGTGTGCTA 45628
QY 1000 TGACATGATGATTTGGCGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAAGGA 1059
    |||||||
Db 45627 TGACATGATGATTTGGCGCTCAAGAGTGTCCGATGCTCTGTGGCTCCAAAAGGA 45568
QY 1060 CAGGATCTTCGAAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
    |||||||
Db 45567 CAGGATCTTCGAAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 45508
QY 1120 CTGGACTCCCATTCACATTTACATCATTAAGCCTTGTTACATCCAGAACTAC 1179
    |||||||
Db 45507 CTGGACTCCCATTCACATTTACATCATTAAGCCTTGTTACATCCAGAACTAC 45448
QY 1180 GTTCCAGACTGTTTCTTGGGACTTCTGATGCTTATAGTTACAAACAGCTGCTCAA 1239
    |||||||
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QY 1240 CCCAGTCTTTATGATCTGATGAAACCTCAACAGATGCTGAGAGTCTGTAT 1299
    |||||||
Db 45387 CCCAGTCTTTATGATCTGATGAAACCTCAACAGATGCTGAGAGTCTGTAT 45328
QY 1300 CCCAACCTTCTTCCACATTTGAGCAACAAACCTCCACTCGAATTCGTAGAACTAGAGA 1359
    |||||||
Db 45327 CCCAACCTTCTTCCACATTTGAGCAACAAACCTCCACTCGAATTCGTAGAACTAGAGA 45268
QY 1360 CCACCCCTCCAGGCGCAATTCAGTGTAGTAAGTAATATCATCAG 1402
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Db 45267 CCACCCCTCCAGGCGCAATTCAGTGTAGTAAGTAATATCATCAG 45225

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RESULT 7

HSOPRMI2 1598 bp DNA PRI 02-DEC-1997

AUTHORS
TITLE
JOURNAL

COMMENT

Sims, S.
Direct Submission
Submitted (15-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jul 22, 2000 this sequence version replaced g1:8977775.
----- Genome Center

Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba157m8

----- Summary Statistics
Sequencing program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 102271 bases at least Q40
Consensus quality: 110329 bases at least Q30
Consensus quality: 115261 bases at least Q20
Insert size: 120669; sum-of-contigs
Quality coverage: 3.24x in Q20 bases; sum-of-contigs quality
coverage: 2.68x in Q20 bases; agarose-tp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1      1459: contig of 1459 bp in length
*      1460 1559: gap of 100 bp
*      1560 3320: contig of 1761 bp in length
*      3321 3420: gap of 100 bp
*      3421 5562: contig of 2142 bp in length
*      5563 5662: gap of 100 bp
*      5663 9774: contig of 4112 bp in length
*      9775 9874: gap of 100 bp
*      9875 11521: contig of 1647 bp in length
*      11522 11621: gap of 100 bp
*      11622 14784: contig of 3163 bp in length
*      14785 14884: gap of 100 bp
*      14885 16929: contig of 2045 bp in length
*      16930 17029: gap of 100 bp
*      17030 21195: contig of 4166 bp in length
*      21196 21295: gap of 100 bp
*      21296 22547: contig of 1252 bp in length
*      22548 22647: gap of 100 bp
*      22648 28063: contig of 5416 bp in length
*      28064 28163: gap of 100 bp
*      28164 30406: contig of 2243 bp in length
*      30407 30506: gap of 100 bp
*      30507 32053: contig of 1547 bp in length
*      32054 32153: gap of 100 bp
*      32154 34236: contig of 2083 bp in length
*      34237 34336: gap of 100 bp
*      34337 36558: contig of 2222 bp in length
*      36559 36658: gap of 100 bp
*      36659 38408: contig of 1750 bp in length
*      38409 38508: gap of 100 bp
*      38509 40660: contig of 2152 bp in length
*      40661 40760: gap of 100 bp
*      40761 42115: contig of 1355 bp in length
*      42116 42215: gap of 100 bp
*      42216 45404: contig of 3189 bp in length
*      45405 45504: gap of 100 bp
*      45505 47767: contig of 2263 bp in length
*      47768 47867: gap of 100 bp
*      47868 50333: contig of 2466 bp in length
*      50334 50433: gap of 100 bp

```

FEATURES

SOURCE

```

*      50434 53910: contig of 3477 bp in length
*      53911 54010: gap of 100 bp
*      54011 55124: contig of 1114 bp in length
*      55125 55224: gap of 100 bp
*      55225 57215: contig of 1991 bp in length
*      57216 57315: gap of 100 bp
*      57316 58382: contig of 1067 bp in length
*      58383 58482: gap of 100 bp
*      58483 80755: contig of 22273 bp in length
*      80756 80855: gap of 100 bp
*      80856 81866: contig of 1011 bp in length
*      81867 81966: gap of 100 bp
*      81967 85210: contig of 3244 bp in length
*      85211 85310: gap of 100 bp
*      85311 87074: contig of 1764 bp in length
*      87075 87174: gap of 100 bp
*      87175 91511: contig of 4337 bp in length
*      91512 91611: gap of 100 bp
*      91612 92650: contig of 1039 bp in length
*      92651 92750: gap of 100 bp
*      92751 95618: contig of 2868 bp in length
*      95619 95718: gap of 100 bp
*      95719 97558: contig of 1840 bp in length
*      97559 97658: gap of 100 bp
*      97659 100174: contig of 2516 bp in length
*      100175 100274: gap of 100 bp
*      100275 101789: contig of 1515 bp in length
*      101790 101889: gap of 100 bp
*      101890 103053: contig of 1164 bp in length
*      103054 103153: gap of 100 bp
*      103154 106517: contig of 3364 bp in length
*      106518 106617: gap of 100 bp
*      106618 107662: contig of 1045 bp in length
*      107663 107762: gap of 100 bp
*      107763 110688: contig of 2926 bp in length
*      110689 110788: gap of 100 bp
*      110789 115340: contig of 4552 bp in length
*      115341 115440: gap of 100 bp
*      115441 124569: contig of 9129 bp in length.

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LOCATION/Qualifiers

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/db_xref="taxon:9606"
/chromosome="6"
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/clone_1kb="RP11-11.1"
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fragment_chain:1"
1560..3320
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fragment_chain:1"
3421..5562
/note="assembly-fragment:00697
fragment_chain:1"
5663..9774
/note="assembly-fragment:01147
fragment_chain:1"
9875..11521
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fragment_chain:2"
11622..14784
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/note="assembly-fragment:00007
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21296..22547
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misc_feature      42216..45404
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Matches 526; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY      302 TGCTCCCGCAGCAGCCAGCCCGCTCTCGGTGCTCACTTCCCACTAGATGGCAACCTG 361
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            Young, G., Zainoun, J., Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Jun 14, 2000 this sequence version replaced gi:7342168.
            All repeats were identified using RepeatMasker:
            Smit, A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIRB
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
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            Center Project name: L8135
            Center clone name: 306_O_7
            ----- Summary Statistics
            Sequencing vector: M13; M77815; 100% of reads
            Assembly program: Phrap; version 0.960731
            Consensus quality: 172491 bases at least Q40
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Insert size: 180348; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs

* NOTE: This is a working draft sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* turns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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*	6574	6673:	gap of 100 bp	
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*	9234	9333:	gap of 100 bp	
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 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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 JOURNAL Unpublished
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 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission

TITLE
 JOURNAL
 COMMENT
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 14, 2000 this sequence version replaced gl:7342168.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 Project Information
 Center project name: 18135
 Center clone name: 306_O_
 Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 172491 bases at least Q40
 Consensus quality: 177577 bases at least Q30
 Consensus quality: 179485 bases at least Q20
 Insert size: 188000; agarose-fp
 Insert size: 180348; sum-of-ctnigs
 Quality coverage: 4.4 in Q20 bases; agarose-fp
 Quality coverage: 4.6 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently

FEATURES
 source
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
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VERSION
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rhesus monkey.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.

REFERENCE
AUTHORS Miller G.M. and Madras B.K.
TITLE Cloning of the Macaca mulatta mu opioid receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1203)
AUTHORS Miller G.M. and Madras B.K.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2000) Neurochemistry, New England Regional
Primate Research Center, Harvard Medical School, One Pine Hill
Drive, Southborough, MA 01772, USA
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EETAPLP"

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QY 736 TCGATACATTTGAGTGTGCGACCCCTGCAAGGCTTAGATTTCCGTAATGCCGAATGC 795
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DB 498 TCGATACATTTGAGTGTGCGACCCCTGCAAGGCTTAGATTTCCGTAATGCCGAATGC 557
QY 796 CAAATATATCAATGCTGCAACTGATCCCTCTTACGATTTGCTTCTCTTAATGTT 855
|||||
DB 558 CAAATATATCAATGCTGCAACTGATCCCTCTTACGATTTGCTTCTCTTAATGTT 617
QY 856 CATGCTACAAACAAATACAGGCAAGTTCAT 888
|||||
DB 618 CATGCTACAAACAAATACAGGCAAGTTCAT 650

RESULT 13
HSOPRM11
LOCUS HSOPRM11 305 bp DNA PRI 02-DEC-1997
DEFINITION Homo sapiens mu opioid receptor (OPRM1) gene, partial cds, exon 1.
ACCESSION AF024515
VERSION AF024515.1 GI:2655101
KEYWORDS
SEGMENT 1 of 3
SOURCE human.

Query Match 13.4% Score 215; DB 11; Length 3759;
 Best Local Similarity 99.7%; Pred. No. 4.3e-11;
 Matches 335; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

44 GCACAGGAGATGTCAGATGCTGAGTGGTCCCTCCGCTGAGCGCTCTGTCTC 103
 |||||||
 Db 3424 GCACAGGAGATGTCAGATGCTGAGTGGTCCCTCCGCTGAGCGCTCTGTCTC 3483
 |||||||
 QY 104 AGCCAGAGCTGTTCTGTAAAGAAACAGCAGAGCTGTGGACGGCGGCGAAAGAGCGGC 163
 |||||||
 Db 3484 AGCCAGAGCTGTTCTGTAAAGAAACAGCAGAGCTGTGGACGGCGGCGAAAGAGCGGC 3543
 |||||||
 QY 164 TGAGGCGGTTGGAAACCGGAAAGTGTGGTGTCTCTGCTACCTGCGACAGC-GTGGCCG 222
 |||||||
 Db 3544 TGAGGCGGTTGGAAACCGGAAAGTGTGGTGTCTCTGCTACCTGCGACAGCAGCGGCGCCG 3603
 |||||||
 QY 223 CCCGCGCTCAGTACATGACAGCAGCGCTGCCCCAGACCGCCAGCAATTCGACTGA 282
 |||||||
 Db 3604 CCCGCGCTCAGTACATGACAGCAGCGCTGCCCCAGACCGCCAGCAATTCGACTGA 3663
 |||||||
 QY 283 TGCTTGGCTGACTCAAGTCTCTCCAGACACCGCCGCTTCTGTCACTGTCTC 342
 |||||||
 Db 3664 TGCTTGGCTGACTCAAGTCTCTCCAGACACCGCCGCTTCTGTCACTGTCTC 3723
 |||||||
 QY 343 CCACCTAGATGCAACCTGTCCGACCCCATGGGCTC 378
 |||||||
 Db 3724 CCACCTAGATGCAACCTGTCCGACCCCATGGGCTC 3759
 |||||||

RESULT 15
 HSDJ402L9
 LOCUS
 DEFINITION Human DNA sequence from clone RP3-402L9 on chromosome 6q25-26.1. Contains the 3' end of the gene for mu opiate receptor (MOR1), the 3' end of the gene KIAA0403, ESTs, STS and GSSs, complete sequence.

ACCESSION AL132774
 VERSION AL132774.20 GI:6706887
 KEYWORDS HMG; KIAA0403; MOR1; opiate receptor.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 98104)
 Phillimore, B.
 Direct Submission
 Submitted (14-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Jan 16, 2000 this sequence version replaced gi:6691954.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 RP3-402L9 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see
<http://bacpac.med.buffalo.edu/>
 VECTOR: PCYPC2

This sequence is the entire insert of clone RP3-402L9 This sequence

was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 5 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Ch6>.
 Location/Qualifiers

FEATURES
 source
 1..98104
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="q25-26.1"
 /clone="RP3-402L9"
 /clone_1lb="RPCI-3"
 199..573
 /note="match: GSS: Em:AQ085222"
 709..1171
 /note="MER41A repeat: matches 1..467 of consensus"
 1188..3645
 /note="MER41-internal repeat: matches 1415..3944 of consensus"
 2966..4247
 /note="MER51-internal repeat: matches 3576..4921 of consensus"
 3866..4332
 /note="MER57-internal repeat: matches 3355..3834 of consensus"
 4329..4383
 /note="MER57-internal repeat: matches 2777..2834 of consensus"
 4380..4455
 /note="MER57-internal repeat: matches 2549..2626 of consensus"
 4383..4511
 /note="HURRS-P3b repeat: matches 3150..3283 of consensus"
 4511..5898
 /note="MER57-internal repeat: matches 305..720 of consensus"
 6493..6567
 /note="LIMA10 repeat: matches 6246..6319 of consensus"
 6932..6971
 /note="20 copies 2 mer tg 100% conserved"
 7746..8055
 /note="Alu repeat: matches 1..311 of consensus"
 8280..8683
 /note="match: GSS: Em:AQ45108"
 8896..9203
 /note="AluYb8 repeat: matches 1..316 of consensus"
 9384..9675
 /note="LTR40b repeat: matches 151..460 of consensus"
 9878..10129
 /note="HERV40 repeat: matches 5247..5505 of consensus"
 10234..10306
 /note="HERV40 repeat: matches 5175..5252 of consensus"
 10611..11070
 /note="HERV40 repeat: matches 4582..5031 of consensus"
 11083..11147
 /note="HERV40 repeat: matches 2597..2660 of consensus"
 11596..12264
 /note="HERV40 repeat: matches 1431..2113 of consensus"
 12402..12690
 /note="AluYb repeat: matches 6..294 of consensus"
 12414..12871
 /note="match: GSS: Em:AQ040924"
 13448..13753
 /note="AluX repeat: matches 5..312 of consensus"
 14486..14736
 /note="LTR40a repeat: matches 151..480 of consensus"
 14998..15027
 /note="15 copies 2 mer gt 100% conserved"
 15818..16598
 /note="match: STS: Em:L25119"
 <15822..16936
 /gene="d0402L9.1"
 /note="match: CDNAS: Em:U35424 Em:U89677 Em:U19380

```

Em:D16349 Em:L38645 Em:L29301 Em:L20684 Em:U26915
Em:L25119 Em:L13069"
/evidence-not experimental
/product="d440219.1 (mu opiate receptor (MOR1))"
15822..16936
/gene="d440219.1"
<15822..15860
/gene="d440219.1"
/codon.start=1
/evidence-not experimental
/product="d440219.1 (mu opiate receptor (MOR1))"
/protein_id="CAB/6846.1"
/db_xref="GI:7161755"
/translacion="LENIKAEAPLP"
15861..16260
/gene="d440219.1"
/note="match: STS: Em:G11298"
16869..16874
/gene="d440219.1"
complement(19456..20016)
/note="match: GSS: Em:AQ373438"
19965..20256
/note="MER61E repeat: matches 341..635 of consensus"
20365..20430
/note="MER61E repeat: matches 99..160 of consensus"
20442..20518
/note="LTR25 repeat: matches 255..333 of consensus"
20658..21195
/note="MER41B repeat: matches 1..542 of consensus"
complement(21441..21938)
/note="match: GSS: Em:B70321"
22930..23240
/note="Aluya5 repeat: matches 1..311 of consensus"
23970..24259
/note="Aluya5 repeat: matches 2..294 of consensus"
26151..26633
/note="LTR2 repeat: matches 3..449 of consensus"
26970..27025
/note="28 copies 2 mer ca 82% conserved"
27305..27606
/note="Aluya repeat: matches 1..304 of consensus"
27794..27923
/note="65 copies 2 mer ta 58% conserved"
29979..30286
/note="Aluy repeat: matches 1..308 of consensus"
30392..30527
/note="L2 repeat: matches 2114..2248 of consensus"
30530..30665
/note="LIM4 repeat: matches 5679..5792 of consensus"
30772..31062
/note="LIM4 repeat: matches 4591..4911 of consensus"
31187..31284
complement(31359..31786)
/note="match: GSS: Em:AQ170692"
complement(31732..32230)
/note="match: GSS: Em:AQ600634"
complement(31826..32245)
/note="match: GSS: Em:AQ440598"
31830..32209
/note="match: GSS: Em:AQ039738"
32280..32753
/note="match: GSS: Em:AQ433448"
32326..32616
/note="Alux repeat: matches 1..290 of consensus"
32617..32678
/note="31 copies 2 mer ta 83% conserved"
34097..34271
/note="MIR repeat: matches 75..262 of consensus"
complement(34529..35091)
/note="match: GSS: Em:AQ896445"
35219..35380
/note="MIR repeat: matches 11..212 of consensus"

repeat_region 35487..35622
/note="MER5B repeat: matches 30..157 of consensus"
repeat_region 35698..36377
/note="LTR8 repeat: matches 1..691 of consensus"
repeat_region 37467..37768
/note="Alux repeat: matches 1..303 of consensus"
repeat_region 38174..38210
/note="tRNA-Glu-GAG repeat: matches 1..37 of consensus"
repeat_region 38608..39053
/note="MER42 repeat: matches 1..504 of consensus"
repeat_region 39278..39978
/note="MER50 repeat: matches 1..734 of consensus"
repeat_region 40338..40512

Query Match 13.0%; Score 209; DB 66; Length 98104;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 TCACCTGAAATCTGAGACAGAACTGCTCCGTTCCCTAACAGGGTCTCATGCAAT 1458
|||||
Db 15818 TCACCTGAAATCTGAGACAGAACTGCTCCGTTCCCTAACAGGGTCTCATGCAAT 15877
|||||
QY 1459 CCGACCTTCACCAAGCTTAGAGCCACCATGATGTGGAAGCAGTTCCTCAAGATG 1518
|||||
Db 15878 CCGACCTTCACCAAGCTTAGAGCCACCATGATGTGGAAGCAGTTCCTCAAGATG 15937
|||||
QY 1519 GTAGAGGCTCTATCTCTAGAGAAAGTGCCTTTAGCTATCCACCTCTTCCTC 1578
|||||
Db 15938 GTAGAGGCTCTATCTCTAGAGAAAGTGCCTTTAGCTATCCACCTCTTCCTC 15997
|||||
QY 1579 TCTGGCCACTCTGCTCTGCACATTAGAGG 1607
|||||
Db 15998 TCTGGCCACTCTGCTCTGCACATTAGAGG 16026
|||||

RESULT 16
G53082 520 bp DNA STS 30-MAR-2000
LOCUS SHGC-84785 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G53082
ACCESSION G53082.1 GI:5224409
VERSION
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshgc.stanford.edu
Primer A: TTACCTCCCTCTTCATCTC
Primer B: ACTGTCCCACTTAGATGCGAAC
STS size: 307
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplifrag Gold Polymerase: 0.07 units/ul

```

Total Vol: 5 u1

Buffer:

MgCl₂: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the Rpl11 BAC library. Designed and developed at the Stanford Human Genome Center.

FEATURES

Location/Qualifiers

1..520

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6"

/clone_lib="Human"

STS

primer_bind 67..373

primer_bind 67..89

complement(351..373)

BASE COUNT 101 a 154 c 153 g 112 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-106;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12.9%; Score 207; DB 91; Length 520;

Query 322 CGTTTCCTGGGTCACTTGTCCCACTAGATGCGACCTGTCGCCACCATCGGTCCGAA 381

Db 387 CGTTTCCTGGGTCACTTGTCCCACTAGATGCGACCTGTCGCCACCATCGGTCCGAA 328

Query 382 CGGACCGACCTGGGCGGAGAGAGACAGCCTGTCGCCACCGACATGCTCCATGAT 441

Db 327 CGGACCGACCTGGGCGGAGAGAGACAGCCTGTCGCCACCGACATGCTCCATGAT 268

Query 442 CACGCGCATCAGATGATGCGCTCTACTCCATGATGATGATGATGATGATGATGAT 501

Db 267 CACGCGCATCAGATGATGCGCTCTACTCCATGATGATGATGATGATGATGATGAT 208

Query 502 CTTCCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528

Db 207 CTTCCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181

RESULT 17

AF100548

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

CDS

<1..>293

/codon_start=1

/product="mu-opioid receptor"

/protein_id="AF04722.1"

/db_xref="GI:6165841"

/translation="LRRITRMVAVVAVAVICWPIPIHVIILALVITPPTFTVSW
HFCIALGYTMSCLPVLVAFVLDENFRFRFCFICPIPTSSVIEQNSRIRHNTA"

BASE COUNT

75 a 79 c 56 g 83 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 8.9e-69;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8.8%; Score 141; DB 11; Length 293;

Query 1172 GAACATACGTTCCAGACTGTTCTTGGACACTTGTGCTAGCTACACAAACAGC 1231

Db 106 GAACATACGTTCCAGACTGTTCTTGGACACTTGTGCTAGCTACACAAACAGC 165

Query 1232 TGCCTCAACCCAGTCCTTATGATTCGTGATGAACAACTCAACGATGCTCAGAG 1291

Db 166 TGCCTCAACCCAGTCCTTATGATTCGTGATGAACAACTCAACGATGCTCAGAG 225

Query 1292 TTCTGTATCCCAACCTCTCC 1312

Db 226 TTCTGTATCCCAACCTCTCC 246

RESULT 18

G11298

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

Unpublished (1995)

Contact: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 415/7259687

Fax: 415/7259689

Email: myers@shgc.stanford.edu

Primer A: CATGCCATTCGACCTTC

Primer B: AGGCATTTCTAGAGAAATAGAGC

STS size: 101

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Tag Polymerase: 0.05 units/u1

Total Vol: 10 u1

Buffer:

MgCl₂: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from L25119 -- Unigene.
Location/Qualifiers

FEATURES
source 1..400
/organism="Homo sapiens"
STS
primer_bind 9..109
primer_bind 9..26
primer_bind complement(85..109)
BASE COUNT 122 a 83 c 83 g 106 t
ORIGIN

Query Match 7.1%; Score 115; DB 91; Length 400;
Best Local Similarity 99.4%; Pred. No. 6,7e-54;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1442 CAGGCTCATGCGATTCGACCTTACACAGCTTAGAAGCCACCATTATGTGGAAGCA 1501
|||||
Db 1 CAGGCTCATGCGATTCGACCTTACACAGCTTAGAAGCCACCATTATGTGGAAGCA 60
QY 1502 GGTGCTTCAAGAAATGTGTAGAGAGCTCTAATCTCTAGAGAAAGTGCCTTTAGGTC 1561
|||||
Db 61 GGTGCTTCAAGAAATGTGTAGAGAGCTCTAATCTCTAGAGAAAGTGCCTTTAGGTC 120
QY 1562 ATCCACCTCTTCCCTCTGCGCAGCTGCTGCGACATTAGAG 1607
|||||
Db 121 ATCCACCTCTTCCCTCTGCGCAGCTGCTGCGACATTAGAG 166

RESULT 19
LOCUS G13228 400 bp DNA SMS 20-DEC-1995
DEFINITION human STS UTR-9720.
ACCESSION G13228
VERSION G13228.1 GI:1127337
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human STS derived from miscellaneous published sequences.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Homnidae; Homo.
1 (bases 1 to 400)
Hudson, T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped STS
Unpublished (1995)

JOURNAL COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CATGCCATCCGACCTTC
Primer B: AGGCACTTCTCTAGAGAAATTAGAC
STS size: 101
PCR profile:

Presoak:
Denaturation: 56 degrees C
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Derived from genbank accession L25119.
Location/Qualifiers

FEATURES
source 1..400
/organism="Homo sapiens"
STS
primer_bind 9..109
primer_bind 9..26
primer_bind complement(85..109)
BASE COUNT 122 a 83 c 83 g 106 t
ORIGIN

Query Match 7.1%; Score 115; DB 91; Length 400;
Best Local Similarity 99.4%; Pred. No. 6,7e-54;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1442 CAGGCTCATGCGATTCGACCTTACACAGCTTAGAAGCCACCATTATGTGGAAGCA 1501
|||||
Db 1 CAGGCTCATGCGATTCGACCTTACACAGCTTAGAAGCCACCATTATGTGGAAGCA 60
QY 1502 GGTGCTTCAAGAAATGTGTAGAGAGCTCTAATCTCTAGAGAAAGTGCCTTTAGGTC 1561
|||||
Db 61 GGTGCTTCAAGAAATGTGTAGAGAGCTCTAATCTCTAGAGAAAGTGCCTTTAGGTC 120
QY 1562 ATCCACCTCTTCCCTCTGCGCAGCTGCTGCGACATTAGAG 1607
|||||
Db 121 ATCCACCTCTTCCCTCTGCGCAGCTGCTGCGACATTAGAG 166

RESULT 20
LOCUS HSOPRM13 669 bp DNA PRI 02-DEC-1997
DEFINITION Homo sapiens mu opiodid receptor (OPRM1) gene, 3'UTR, partial
sequence:
ACCESSION AF024517 GI:2655103
VERSION AF024517.1
KEYWORDS
SEGMENT
SOURCE human.
3 of 3
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
1 (bases 1 to 669)
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A.
and Uhl, G.R.
Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment
FEBS Lett. 338 (2), 217-222 (1994)
2 (bases 1 to 669)
Bare, L.A., Mansson, E. and Yang, D.
Expression of two variants of the human mu opiodid receptor mRNA in
SK-N-SH cells and human brain
FEBS Lett. 354 (2), 213-216 (1994)
3 (bases 1 to 669)
Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M.,
Linnoila, M. and Goldman, D.
Mu opiodid receptor gene variants: lack of association with alcohol
dependence
Mol. Psychiatry 2 (6), 490-494 (1997)
4 (bases 1 to 669)
Bergen, A.W., Kokoszka, J. and Goldman, D.
Direct Submission
Submitted (11-SEP-1997) Neurogenetics, NIMH/NIH, 12501 Washington

JOURNAL MEDLINE
REFERENCE 98060615
AUTHORS Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M.,
Linnoila, M. and Goldman, D.
Mu opiodid receptor gene variants: lack of association with alcohol
dependence
Mol. Psychiatry 2 (6), 490-494 (1997)
4 (bases 1 to 669)
Bergen, A.W., Kokoszka, J. and Goldman, D.
Direct Submission
Submitted (11-SEP-1997) Neurogenetics, NIMH/NIH, 12501 Washington

COMMENT Avenue, Rockville, MD 20852, USA
30 US Caucasian and North American Indian chromosomes were directly
sequenced at the OPRM1 locus, 3'UTR.

FEATURES
Source Location/Qualifiers

1. .669

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/map="6q24-q25"

order(AF024515.1:<1. .305,AF024516.1:1. .340,

AF024516.1:1.114. .1598,1. .>669)

/product="mu opioid receptor"

order(AF024515.1:<1. .305,AF024516.1:1. .1598,1. .>669)

/gene="OPRM1"

/note="mu opioid receptor locus"

<1. .>669

/gene="OPRM1"

56

/note="OPRM1"

/citation="11"

/replace="a"

398

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation="11"

/replace="a"

443

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation="11"

/replace="a"

513

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation="11"

/replace="a"

594

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation="11"

/replace="a"

622

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation="11"

/replace="n"

131 c

205 t

BASE COUNT

202 a

131 g

ORIGIN

131 c

205 t

BASE COUNT

202 a

131 g

ORIGIN

131 c

205 t

BASE COUNT

202 a

131 g

ORIGIN

131 c

205 t

BASE COUNT

202 a

131 g

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

20050861

2 (bases 1 to 1415)

Simon,E.J.,

Onopriashvili,I.,

Andria,M.L.,

Vilim,F.S.,

Hiller,J.M. and

Simon,E.J.

The bovine mu-opioid receptor: cloning of cDNA and pharmacologic

characterization of the receptor expressed in mammalian cells

Brain Res. Mol. Brain Res. 73 (1-2), 129-137 (1999)

Submitted (13-FEB-1997) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

3 (bases 1 to 1415)

Simon,E.J.,

Vilim,S.,

Andria,M.,

Onopriashvili,I. and

Hiller,J.M.

Submitted (26-MAR-1999) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

Sequence update by submitter

On Mar 26, 1999 this sequence version replaced gi:1881730.

REMARK

COMMENT

FEATURES

Source

1. .1415

/organism="Bos taurus"

/db_xref="taxon:9913"

/tissue_type="striatum"

156. .1361

/note="G-protein coupled receptor"

/codon_start=1

/product="mu opioid receptor"

/protein_id="AAB9477.2"

/db_xref="GI:4521326"

/translacion="MDSGAVPTNANCTDFTPHSSCPSPSSWVNFSLGSLSD

PCGNRTLEIGSDRLCPGAGSPWITRIIIMATLSIVCVGLFQNFVIMVIVATYK

KTAIRYIFNLADALATSLTPQSNVYIMGTFPGLIKIVISIDYIMNFISIT

LCITMSVDRIYAVCHPVKALDLRPNRNKKIINICWMLISAGLPVMTATKRGSI

DCITREHPMTWENMLKICVFIFAFIMPLIITVCGIMLRKSVRMISGSEKXR

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LEAETTPLP"

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

309 g

339 t

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Cetartiodactyla, Ruminantia, Pecora: Bovidae;
Bovidae; Bovinae: Bos.

1 (bases 1 to 1415)

Simon,E.J.,

Onopriashvili,I.,

Andria,M.L.,

Vilim,F.S.,

Hiller,J.M. and

Simon,E.J.

The bovine mu-opioid receptor: cloning of cDNA and pharmacologic

characterization of the receptor expressed in mammalian cells

Brain Res. Mol. Brain Res. 73 (1-2), 129-137 (1999)

Submitted (13-FEB-1997) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

3 (bases 1 to 1415)

Simon,E.J.,

Vilim,S.,

Andria,M.,

Onopriashvili,I. and

Hiller,J.M.

Submitted (26-MAR-1999) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

Sequence update by submitter

On Mar 26, 1999 this sequence version replaced gi:1881730.

REMARK

COMMENT

FEATURES

Source

1. .1415

/organism="Bos taurus"

/db_xref="taxon:9913"

/tissue_type="striatum"

156. .1361

/note="G-protein coupled receptor"

/codon_start=1

/product="mu opioid receptor"

/protein_id="AAB9477.2"

/db_xref="GI:4521326"

/translacion="MDSGAVPTNANCTDFTPHSSCPSPSSWVNFSLGSLSD

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LCITMSVDRIYAVCHPVKALDLRPNRNKKIINICWMLISAGLPVMTATKRGSI

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NLRITRMVLVVAFTVCMPTPHIIVYITAIITIPETTTQTVSWHFCIALGTNSCL

NPVLVAFLEDFKRFRCFIPISSTIEQNSTRIKNTIDHPSITANTVDTNQLN

LEAETTPLP"

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

309 g

339 t

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

309 g

339 t

BASE COUNT

337 a

430 c

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini; Hominiidae: Homo.

1 (bases 1 to 77313)

Bliren,B.,

Linton,L.,

Nusbaum,C. and

Lander,E.

Homo sapiens chromosome 11, clone RP11-310M4

Submitted (13-FEB-1997) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

3 (bases 1 to 1415)

Simon,E.J.,

Vilim,S.,

Andria,M.,

Onopriashvili,I. and

Hiller,J.M.

Submitted (26-MAR-1999) Psychiatry, NYU Med. Center, 550 First

Ave., New York, NY 10016, USA

Sequence update by submitter

On Mar 26, 1999 this sequence version replaced gi:1881730.

REMARK

COMMENT

FEATURES

Source

1. .1415

/organism="Bos taurus"

/db_xref="taxon:9913"

/tissue_type="striatum"

156. .1361

/note="G-protein coupled receptor"

/codon_start=1

/product="mu opioid receptor"

/protein_id="AAB9477.2"

/db_xref="GI:4521326"

/translacion="MDSGAVPTNANCTDFTPHSSCPSPSSWVNFSLGSLSD

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KTAIRYIFNLADALATSLTPQSNVYIMGTFPGLIKIVISIDYIMNFISIT

LCITMSVDRIYAVCHPVKALDLRPNRNKKIINICWMLISAGLPVMTATKRGSI

DCITREHPMTWENMLKICVFIFAFIMPLIITVCGIMLRKSVRMISGSEKXR

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NPVLVAFLEDFKRFRCFIPISSTIEQNSTRIKNTIDHPSITANTVDTNQLN

LEAETTPLP"

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

309 g

339 t

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

309 g

339 t

BASE COUNT

337 a

430 c

309 g

339 t

ORIGIN

430 c

JOURNAL
REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 77313)
Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bida, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeRellano, K., Dewar, K., Domino, M., Doyle, M., Fennestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Gargan, J.,
Garday, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howard, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, E., Lehoczy, J., Levine, R., Lien, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McCurt, A., McKernan, K.,
McNeesters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6922183.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6177
Center clone name: 310_M4
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
* 876 975: contig of 875 bp in length
* 976 1889: contig of 914 bp in length
* 1890 1989: gap of 100 bp
* 1990 2894: contig of 905 bp in length
* 2895 2994: gap of 100 bp
* 2995 3861: contig of 867 bp in length
* 3862 3961: gap of 100 bp
* 3962 4832: contig of 871 bp in length
* 4833 4932: gap of 100 bp
* 4933 5840: contig of 908 bp in length
* 5841 5940: gap of 100 bp
* 5941 6823: contig of 883 bp in length
* 6824 6923: gap of 100 bp
* 6924 7830: contig of 907 bp in length
* 7831 7930: gap of 100 bp
* 7931 8844: contig of 914 bp in length
* 8845 8944: gap of 100 bp
* 8945 9870: contig of 926 bp in length
* 9871 9970: gap of 100 bp
* 9971 10835: contig of 865 bp in length
* 10836 10935: gap of 100 bp
* 10936 11840: contig of 905 bp in length
* 11841 11940: gap of 100 bp
* 11941 12816: contig of 876 bp in length
* 12817 12916: gap of 100 bp
* 12917 13799: contig of 883 bp in length

13800 13899: gap of 100 bp
* 13900 14784: contig of 885 bp in length
* 14785 14884: gap of 100 bp
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* 15777 15876: gap of 100 bp
* 15877 16773: contig of 897 bp in length
* 16774 16873: gap of 100 bp
* 16874 17772: contig of 899 bp in length
* 17773 17872: gap of 100 bp
* 17873 18790: contig of 918 bp in length
* 18791 18890: gap of 100 bp
* 18891 19745: contig of 855 bp in length
* 19746 19845: gap of 100 bp
* 19846 20749: contig of 904 bp in length
* 20750 20849: gap of 100 bp
* 20850 21718: contig of 869 bp in length
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* 21819 22692: contig of 874 bp in length
* 22693 22792: gap of 100 bp
* 22793 23653: contig of 861 bp in length
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* 23754 24628: contig of 876 bp in length
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* 24730 25603: contig of 874 bp in length
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* 25704 26550: contig of 847 bp in length
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* 26651 27562: contig of 912 bp in length
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* 28674 29587: contig of 914 bp in length
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* 37515 37614: gap of 100 bp
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* 38465 38564: gap of 100 bp
* 38565 39516: contig of 952 bp in length
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* 44721 45616: contig of 896 bp in length
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* 51568 51667: contig of 913 bp in length
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* 53517 53517: contig of 892 bp in length
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* 54607 55490: contig of 884 bp in length
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* 57410 57509: gap of 100 bp
* 57510 58420: contig of 911 bp in length
* 58421 58520: gap of 100 bp
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* 62393 62492: gap of 100 bp
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* 63359 63458: gap of 100 bp
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* 66244 66343: gap of 100 bp
* 66344 67219: contig of 876 bp in length
* 67220 67319: gap of 100 bp
* 67320 68229: contig of 910 bp in length
* 68230 68329: gap of 100 bp
* 68330 69241: contig of 912 bp in length
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Best Local Similarity 98.9%: Pred. No. 2e-30; Indels 0; Gaps 0;
Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1399 TCAGCTAGAAAATCGAAGAGCAAACTGCTCGTTCCTTACAGAGGTCATGCCATT 1458
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Oy 1459 CCGACCTTCACCAAGCTTAGAAGCCACATGATGTGGAAGCAGGTTGCTTCAAGATGT 1518
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Db 23133 CCGACCTTCACCAAGCTTAGAAGCCACATGATGTGGAAGCAGGTTGCTTCAAGATGT 23192
Oy 1519 GTAGAGGCTCTAATTCCTAGGAAGTGCCTTTAGGTCATCCAACTCCTT 1574
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Db 23193 GTAGAGGCTCTAATTCCTAGGAAGTGCCTTTAGGTCATCCAACTCCTT 23248

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LOCUS PIGMUOPR 1881 bp mRNA MAM 03-MAR-1999
DEFINITION Sus scrofa mu oploid receptor mRNA, complete cds.
ACCESSION L38645
VERSION L38645.1 GI:2072391
KEYWORDS
SOURCE
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE (bases 1 to 1881)
REFERENCE Pamusch, M.S., Osinski, M.A., Brown, D.R. and Mutaugh, M.P.
AUTHORS The porcine mu oploid receptor: molecular cloning and mRNA
```

JOURNAL distribution in lymphoid tissues
MEDLINE J Neuroimmunol. 90 (2), 192-198 (1998)
REFERENCE 90032385.
AUTHORS 2 (bases 1 to 1881)
TITLE Osinski, M.A.
JOURNAL Direct Submission
Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology,
University of Minnesota, St. Paul, MN 55108, USA 1:553056.
COMMENT On May 6, 1997 this sequence version replaced gi:1553056.
FEATURES
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DCAITFSHPFTMYENLKIYCFITAFIPVLIITVCYGLMLRLKSTRMSGKREKOR
NLRRITRMVLVAVFTVCMPIHIVIIALITIPETQTVSMHFCIALGYNSCL
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LEATPALEP"

BASE COUNT 463 a 533 c 423 g 462 t
ORIGIN

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Best Local Similarity 100.0%: Pred. No. 1e-28;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1298 ATCCCACTC 1308
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Db 1299 ATCCCACTC 1309
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RESULT 24
LOCUS MMOR2 371 bp DNA ROD 08-NOV-1994
DEFINITION Mus musculus mu oploid receptor (MOR) gene, exon 2.
ACCESSION U10559
VERSION U10559.1 GI:565066
KEYWORDS
SEGMENT 2 of 4
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE (bases 10 to 362)
REFERENCE Min, B.H., Augustin, L.B., Felsheim, R.F., Fuchs, J.A. and Loh, H.-F.
AUTHORS Genomic structure analysis of promoter sequence of a mouse mu
TITLE Oploid receptor gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (19), 9081-9085 (1994)
MEDLINE 94377496.
REFERENCE Augustin, L.B.
AUTHORS 2 (bases 1 to 371)
TITLE Direct Submission
JOURNAL Submitted (13-JUN-1994) Lance B. Augustin, Pharmacology, University
of Minnesota, 435 Delaware Street SE, Minneapolis, MN 55455, USA
FEATURES  
source Location/Qualifiers  
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/strain="C57 Black/6"
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10.362
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363.3371
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 25
AF074973 1334 bp mRNA ROD 31-AUG-1999
LOCUS AF074973
DEFINITION Mus musculus mu oploid receptor MOR1D mRNA, alternatively spliced,
complete cds.
AF074973.1 GI:5805152

ACCESSION
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1334)
Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A.,
Rossi,G. and Pasternak,G.W.
Identification and characterization of three new alternatively
spliced mu-oploid receptor isoforms
Mol. Pharmacol. 56 (2), 396-403 (1999)
99348417
JOURNAL
MEDLINE
2 (bases 1 to 1334)
Pan,Y.-X., Xu,J., Man,B.-L., Zuckerman,A.B., Rossi,G.C.,
Leventhal,L. and Pasternak,G.W.
Direct Submision
Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
location/Qualifiers
1.1334
/organism="Mus musculus"
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67.1248
/note="alternatively spliced exon 4"
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/product="mu oploid receptor MOR1D"
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MSVDRYAVCHPVKALDFRTPRNKIVNVCNWLSSAIGLPMVMTATKRGSDICT
LTSHPTWVENLKIICVTFEAFIMPLVITVGLMLILKLSVRLSGSKERDNR
RITRMVLVVAVFVTCWTPPIHIVIIKALITPETFQVSMHFCIALGYTNSCLNP
LVAFIDENFKRCEFCIPSTIEONSARIRONTREHSTANTVDRTHQRPLEPS
S"

BASE COUNT 320 a 397 c 297 g 320 t
ORIGIN

Query Match
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTAGCCAC 419

RESULT 26
AF062753 1423 bp mRNA ROD 10-SEP-1999
LOCUS AF062753
DEFINITION Mus musculus mu oploid receptor variant C mRNA, complete cds.
AF062753.1 GI:5853308

ACCESSION
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1423)
Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A.,
Rossi,G. and Pasternak,G.W.
Identification and characterization of three new alternatively
spliced mu-oploid receptor isoforms
Mol. Pharmacol. 56 (2), 396-403 (1999)
99348417
JOURNAL
MEDLINE
2 (bases 1 to 1423)
Pan,Y.-X., Xu,J., Man,B.-L., Zuckerman,A.B. and Pasternak,G.W.
Direct Submision
Submitted (04-MAY-1998) Department of Neurology, Memorial
Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021,
USA
location/Qualifiers
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/protein_id="A054415.1"
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MSVDRYAVCHPVKALDFRTPRNKIVNVCNWLSSAIGLPMVMTATKRGSDICT
LTSHPTWVENLKIICVTFEAFIMPLVITVGLMLILKLSVRLSGSKERDNR
RITRMVLVVAVFVTCWTPPIHIVIIKALITPETFQVSMHFCIALGYTNSCLNP
LVAFIDENFKRCEFCIPSTIEONSARIRONTREHSTANTVDRTHQRPLEPS
VAOIFGTGYPPTVEKRCCKMRCGRNLLPDDGPRQSESGQLGR"

BASE COUNT 343 a 423 c 317 g 340 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.3e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTAGCCAC 597
|||||
Db 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTAGCCAC 419

RESULT 27
AF074974 1543 bp mRNA ROD 31-AUG-1999
LOCUS AF074974
DEFINITION Mus musculus mu oploid receptor MOR1E mRNA, alternatively spliced,
complete cds.
AF074974.1 GI:5805154

ACCESSION
VERSION
KEYWORDS

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1543)
AUTHORS Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A., Rossi,G. and Pasternak,G.W.
TITLE Identification and characterization of three new alternatively spliced mu-opioid receptor isoforms
JOURNAL Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE 99348417
REFERENCE 2 (bases 1 to 1543)
AUTHORS Pan,Y.X., Xu,J., Wan,B.-L., Zuckerman,A.B., Rossi,G.C., Leventhal,L. and Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, New York, NY 10021, USA

FEATURES
source location/Qualifiers
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ORGVQHPV"

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BASE COUNT 369 a 455 c 345 g 374 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTCACCTTGCTGCGAGATGCTTAGCCAC 597
Db 361 ATGAAGACTGCCACCAACATCTACATTTCACCTTGCTGCGAGATGCTTAGCCAC 419

RESULT 28
LOCUS MM026915 1610 bp mRNA ROD 09-NOV-1995
DEFINITION Mus musculus mu opioid receptor (MOR-1) mRNA, complete cds.
ACCESSION U26915
VERSION U26915.1 GI:1055230
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1610)
REFERENCE Rossi,G.C., Pan,Y.X., Brown,G.P. and Pasternak,G.W.
AUTHORS Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor
JOURNAL FEBS Lett. 369 (2-3), 192-196 (1995)
MEDLINE 95377399
REFERENCE 2 (bases 1 to 1610)
AUTHORS Pan,Y.X.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1995) Yling-xian Pan, Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

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ETAPLP"

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BASE COUNT 373 a 476 c 368 g 393 t
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Best Local Similarity 100.0%; Pred. No. 7.4e-22;
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QY 539 ATGAAGACTGCCACCAACATCTACATTTCACCTTGCTGCGAGATGCTTAGCCAC 597
Db 577 ATGAAGACTGCCACCAACATCTACATTTCACCTTGCTGCGAGATGCTTAGCCAC 635

RESULT 29
LOCUS AF167568 1729 bp mRNA ROD 28-JUN-2000
DEFINITION Mus musculus mu opioid receptor variant F mRNA, complete cds.
ACCESSION AF167568
VERSION AF167568.1 GI:8778197
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1729)
REFERENCE Pan,Y.X., Xu,J., Bolan,E., Chang,A., Mahurter,L., Rossi,G. and Pasternak,G.W.
AUTHORS Isolation and expression of a novel alternatively spliced mu opioid receptor isoform, MOR-1F
JOURNAL FEBS Lett. 466 (2-3), 337-340 (2000)
MEDLINE 20145060
REFERENCE 2 (bases 1 to 1729)
AUTHORS Pan,Y.X., Xu,J., Chang,A., Mahurter,L. and Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2000) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

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 RTRMVLVVAVFIVCMTPIHIVIKALITITPETVQVNSFICIALGINSCLNPV
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 LGANGQKASLDLLELETYSHQDAETNPGPYEGSKACPLAISIVPLT"
 BASE COUNT 417 a 505 c 395 g 412 t
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Query Match 3.7%; Score 59; DB 12; Length 1729;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 597
 Db 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 419

RESULT 30
 LOCUS A68824 2229 bp DNA PAT 06-MAY-1999
 DEFINITION Sequence 1 from Patent WO9802534.
 ACCESSION A68824
 VERSION A68824.1 GI:4759752
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2229)
 Kieffer,B.L., Matthes,H.W., Simonin,F.H., Dierich,A. and Lemeur,M.
 TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS
 MODIFIED
 JOURNAL Patent: WO 9802534-A 22-JAN-1998;
 CENTRE NAT RECH SCIENT (FR)
 Other publication FR 2750825 19980116.
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 ORIGIN

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 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 597
 Db 550 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 608

RESULT 31
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 DEFINITION Mus musculus mu opioid receptor cDNA, complete cds.
 ACCESSION U19380
 VERSION U19380.1 GI:885864
 KEYWORDS

SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2229)
 Kaufman,D.L., Keith,D.E., Anton,B., Tian,J., Magendzo,K.,
 Newman,D.J., Tran,T., Lee,D.S., Wen,C., Xia,Y., Lussis,A.J. and
 Evans,C.J.
 Characterization of the murine mu opioid receptor gene
 JOURNAL J. Biol. Chem. 270 (26), 15877-15883 (1995)
 MEDLINE 95318184
 REFERENCE 2 (bases 1 to 2229)
 Evans,C.C.
 Direct Submission
 JOURNAL Submitted (04-JAN-1995) Christopher J Evans, Psychiatry and
 Biobehavioral Sciences, University of California at Los Angeles,
 UCLA-NPI, 760 Westwood Plaza, Los Angeles, CA 90024-1759, USA
 FEATURES
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 ETAPLP"

CDS

BASE COUNT 562 a 608 c 489 g 570 t
 ORIGIN

Query Match 3.7%; Score 59; DB 12; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 597
 Db 550 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGGCAGATGCTTACCCAC 608

RESULT 32
 LOCUS AC055776 178454 bp DNA HTG 22-JUL-2000
 DEFINITION Mus musculus chromosome 10 clone RP23-11015 map 10, WORKING DRAFT
 SEQUENCE, 21 unordered pieces.
 ACCESSION AC055776
 VERSION AC055776.2 GI:9369492
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 178454)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Mus musculus chromosome 10, clone RP23-11015
 Unpublished
 JOURNAL 2 (bases 1 to 178454)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
 Campolano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

TITLE
JOURNAL
COMMENT

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goylette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPheters, R.,
Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisanic, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessier, S., Theodore, J., Turrell, A., Travers, M., Triggillo, D.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 22, 2000 this sequence version replaced g1:7582600.
All repeats were identified using RepeatMasker:

Slit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L5745

Center clone name: 11.O.15

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 166586 bases at least Q40
Consensus quality: 172885 bases at least Q30
Consensus quality: 175270 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 176454; sum-of-ctrls
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1545: contig of 1545 bp in length
1546 1645: gap of 100 bp
1646 2950: contig of 1305 bp in length
2951 3050: gap of 100 bp
3051 5112: contig of 2062 bp in length
5113 5212: gap of 100 bp
5213 8232: contig of 3020 bp in length
8233 8332: gap of 100 bp
8333 13079: contig of 4747 bp in length
13080 13179: gap of 100 bp
13180 16940: contig of 3761 bp in length
16941 17040: gap of 100 bp
17041 21192: contig of 4152 bp in length
21193 21292: gap of 100 bp
21293 26578: contig of 5286 bp in length
26579 26678: gap of 100 bp
26679 32608: contig of 5930 bp in length
32609 32708: gap of 100 bp
32709 38888: contig of 6180 bp in length
38889 38988: gap of 100 bp
38989 44556: contig of 5568 bp in length

FEATURES

source

44557 44556: gap of 100 bp
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51769 51868: gap of 100 bp
51869 58681: contig of 6813 bp in length
58682 58781: gap of 100 bp
58782 65622: contig of 6841 bp in length
65623 65722: gap of 100 bp
65723 77537: contig of 11815 bp in length
77538 77637: gap of 100 bp
77638 85102: contig of 7465 bp in length
85103 85202: gap of 100 bp
85203 99219: contig of 14017 bp in length
99220 99319: gap of 100 bp
99320 110889: contig of 11570 bp in length
110890 110989: gap of 100 bp
110990 132713: contig of 21724 bp in length
132714 132813: gap of 100 bp
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION     AF266480
VERSION       AF266480.1 GI:8572232
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ORGANISM      sheep.
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               Bovidae; Caprinae; Ovis.
               1 (bases 1 to 193)
REFERENCE
AUTHORS       Thompson, R.C.
TITLE         Ovine Mu Oploid Receptor
JOURNAL
REFERENCE      Unpublished
AUTHORS        2 (bases 1 to 193)
TITLE         Thompson, R.C.
JOURNAL        Direct Submission
               Submitted (10-MAY-2000) Psychiatry, University of Michigan, 4451
               Kresge I, Ann Arbor, MI 48109-0512, USA

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VERSION       AC022855.2 GI:9158694
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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               1 (bases 1 to 77313)
REFERENCE
AUTHORS       Birren, B., Linton, L., Nusbaum, C. and Lander, E.

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TITLE
JOURNAL
REFERENCE
AUTHORS
Homo sapiens chromosome 11, clone RP11-310M4
Unpublished
2 (bases 1 to 77313)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepe, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P.,
Darellano, K., Dewar, K., Domino, M., Doyle, M., Fennestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Gault, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lebeck, J., Levine, R., Liu, C., Liu, G., Locke, K.,
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Roy, A., Santos, R., Severy, P., Spencer, R., Stange-Themann, N.,
Stojanovic, N., Subramanian, A., Talmes, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliou, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.

Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6922183.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WtIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6117
Center clone name: 310_M4

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
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1990 2894: contig of 905 bp in length
2895 2994: gap of 100 bp
2995 3861: contig of 867 bp in length
3862 3961: gap of 100 bp
3962 4832: contig of 871 bp in length
4833 4932: gap of 100 bp
4933 5840: contig of 908 bp in length
5841 5940: gap of 100 bp
5941 6823: contig of 883 bp in length
6824 6923: gap of 100 bp
6924 7830: contig of 907 bp in length
7831 7930: gap of 100 bp
7931 8844: contig of 914 bp in length
8845 8944: gap of 100 bp
8945 9870: contig of 926 bp in length
9871 9970: gap of 100 bp
9971 10835: contig of 865 bp in length
10836 10935: gap of 100 bp
10936 11840: contig of 905 bp in length
11841 11940: gap of 100 bp
11941 12816: contig of 876 bp in length
12817 12916: gap of 100 bp

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* 12917 13799: contig of 883 bp in length
* 13800 13899: gap of 100 bp
* 13900 14784: contig of 885 bp in length
* 14785 14884: gap of 100 bp
* 14885 15776: contig of 892 bp in length
* 15777 15876: gap of 100 bp
* 15877 16773: contig of 897 bp in length
* 16774 16873: gap of 100 bp
* 16874 17772: contig of 899 bp in length
* 17773 17872: gap of 100 bp
* 17873 18790: contig of 918 bp in length
* 18791 18890: gap of 100 bp
* 18891 19745: contig of 855 bp in length
* 19746 19845: gap of 100 bp
* 19846 20749: contig of 904 bp in length
* 20750 20849: gap of 100 bp
* 20850 21718: contig of 869 bp in length
* 21719 21818: gap of 100 bp
* 21819 22692: contig of 874 bp in length
* 22693 22792: gap of 100 bp
* 22793 23653: contig of 861 bp in length
* 23654 23753: gap of 100 bp
* 23754 24629: contig of 876 bp in length
* 24630 24729: gap of 100 bp
* 24730 25603: contig of 874 bp in length
* 25604 25703: gap of 100 bp
* 25704 26550: contig of 847 bp in length
* 26551 26650: gap of 100 bp
* 26651 27562: contig of 912 bp in length
* 27563 27662: gap of 100 bp
* 27663 28573: contig of 911 bp in length
* 28574 28673: gap of 100 bp
* 28674 29587: contig of 914 bp in length
* 29588 29687: gap of 100 bp
* 29688 30564: contig of 877 bp in length
* 30565 30664: gap of 100 bp
* 30665 31568: contig of 904 bp in length
* 31569 31668: gap of 100 bp
* 31669 32538: contig of 870 bp in length
* 32539 32638: gap of 100 bp
* 32639 33543: contig of 905 bp in length
* 33544 33643: gap of 100 bp
* 33644 34549: contig of 906 bp in length
* 34550 34649: gap of 100 bp
* 34650 35551: contig of 902 bp in length
* 35552 35651: gap of 100 bp
* 35652 36514: contig of 863 bp in length
* 36515 36614: gap of 100 bp
* 36615 37514: contig of 900 bp in length
* 37515 37614: gap of 100 bp
* 37615 38464: contig of 850 bp in length
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* 38565 39516: contig of 952 bp in length
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* 39617 40554: contig of 938 bp in length
* 40555 40654: gap of 100 bp
* 40655 41579: contig of 925 bp in length
* 41580 41679: gap of 100 bp
* 41680 42618: contig of 939 bp in length
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* 42719 43623: contig of 905 bp in length
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* 43724 44620: contig of 897 bp in length
* 44621 44720: gap of 100 bp
* 44721 45616: contig of 896 bp in length
* 45617 45716: gap of 100 bp
* 45717 46589: contig of 873 bp in length
* 46590 46689: gap of 100 bp
* 46690 47557: contig of 868 bp in length
* 47558 47657: gap of 100 bp
* 47658 48561: contig of 904 bp in length
* 48562 48661: gap of 100 bp
* 48662 49540: contig of 879 bp in length

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* 49541 49640: gap of 100 bp
* 49641 50554: contig of 914 bp in length
* 50555 50654: gap of 100 bp
* 50655 51567: contig of 913 bp in length
* 51568 51667: gap of 100 bp
* 51668 52525: contig of 858 bp in length
* 52526 52625: gap of 100 bp
* 52626 53517: contig of 892 bp in length
* 53518 53617: gap of 100 bp
* 53618 54506: contig of 889 bp in length
* 54507 54606: gap of 100 bp
* 54607 55490: contig of 884 bp in length
* 55491 55590: gap of 100 bp
* 55591 56432: contig of 842 bp in length
* 56433 56532: gap of 100 bp
* 56533 57409: contig of 877 bp in length
* 57410 57509: gap of 100 bp
* 57510 58420: contig of 911 bp in length
* 58421 58520: gap of 100 bp
* 58521 59404: contig of 884 bp in length
* 59405 59504: gap of 100 bp
* 59505 60391: contig of 887 bp in length
* 60392 60491: gap of 100 bp
* 60492 61436: contig of 945 bp in length
* 61437 61536: gap of 100 bp
* 61537 62392: contig of 856 bp in length
* 62393 62492: gap of 100 bp
* 62493 63358: contig of 866 bp in length
* 63359 63458: gap of 100 bp
* 63459 64302: contig of 844 bp in length
* 64303 64402: gap of 100 bp
* 64403 65258: contig of 856 bp in length
* 65259 65358: gap of 100 bp
* 65359 66243: contig of 885 bp in length
* 66244 66343: gap of 100 bp
* 66344 67219: contig of 876 bp in length
* 67220 67319: gap of 100 bp
* 67320 68229: contig of 910 bp in length
* 68230 68328: gap of 100 bp
* 68330 69241: contig of 912 bp in length
* 69242 69341: gap of 100 bp
* 69342 70259: contig of 918 bp in length

Query Match          3.0%: Score 49; DB 76; Length 77313;
Best Local Similarity 100.0%: Pred. No. 4,1e-16;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1425 CTGCTCGCTGCGCTACAGGCTCATGCGACCTTCACAGG 1473
    |||||
Db 40745 CTGCTCGCTGCGCTACAGGCTCATGCGACCTTCACAGG 40697

RESULT 35
RNU35424      1367 bp      mRNA      ROD      12-OCT-1995
LOCUS        Rattus norvegicus mu opioid receptor mRNA, complete cds.
DEFINITION   U35424
ACCESSION    U35424
VERSION      U35424.1 GI:1017731
KEYWORDS
SOURCE
ORGANISM     Norway rat.
              Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1 (bases 1 to 1367)
AUTHORS     Zastawny,R.L., George,S.R., Nguyen,T., Cheng,R., Tsatsos,J.,
              Briones-Jrblan,R. and O'Dowd,B.F.
              Cloning, characterization, and distribution of a mu-opioid receptor
              in rat brain
JOURNAL     J. Neurochem. 62 (6), 2099-2105 (1994)
MEDLINE     94246380
REFERENCE    2 (bases 1 to 1367)
AUTHORS     O'Dowd,B.F.

```

TITLE Direct Submission
JOURNAL Submitted (05-SEP-1995) Brian F. O'Dowd, Pharmacology, University
of Toronto, 8 Taddle Creek Rd., Toronto, ON M5S 1A8, Canada

FEATURES
Source
Location/Qualifiers
1. 1367
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/db_xref="taxon:10116"
70. 1266
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/protein_id="AA09180.1"
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LNRGLGNDSLCPQSGPSMVAITITMALISYCVGLFNGFLVMYIVRYTKKTA
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MSVDRIYAVCHPVKALDFRTPRNKIVNVCNMISSAIGLPMFMATTKRQSGIDCT
LTFSPHTWENLKLICVETFAFIMPLVILITVCGMLRLKSVRMATSGSKEDNRL
RITRMVLVVAVFVVCWPIHIVIKALITPETTQVSMHCIALGYNSCLNP
LYAFLDENFKRCFRFCIPSTISIEQNSTVRONTREHPSANTVDRTNQLENLEA
ETAPLP"

CDS
170. 1366
/tissue_type="olfactory bulb"
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/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
/db_xref="GI:437672"
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MSVDRIYAVCHPVKALDFRTPRNKIVNVCNMISSAIGLPMFMATTKRQSGIDCT
LTFSPHTWENLKLICVETFAFIMPLVILITVCGMLRLKSVRMATSGSKEDNRL
RITRMVLVVAVFVVCWPIHIVIKALITPETTQVSMHCIALGYNSCLNP
LYAFLDENFKRCFRFCIPSTISIEQNSTVRONTREHPSANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 330 a 434 c 312 g 325 t

Query Match 2.9%; Score 47; DB 12; Length 1367;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
|||||
DB 364 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 410
|||||

RESULT 36
RATMOP10ID 1401 bp mRNA ROD 24-JAN-1994
LOCUS Rat mu opioid receptor mRNA, complete cds.
ACCESSION L22455
VERSION L22455.1 GI:437671
KEYWORDS mu opioid receptor.
SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1401)
Thompson, R.C., Mansour, A., Akil, H. and Watson, S.J.
Cloning and pharmacological characterization of a rat mu opioid
receptor
Neuron 11 (5), 903-913 (1993)
94059560
Location/Qualifiers
1. 1401
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/strain="Sprague-Dawley"
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/sex="male"
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/tissue_1bp="lambda ZAP1 from Stratagene"
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
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MSVDRIYAVCHPVKALDFRTPRNKIVNVCNMISSAIGLPMFMATTKRQSGIDCT
LTFSPHTWENLKLICVETFAFIMPLVILITVCGMLRLKSVRMATSGSKEDNRL
RITRMVLVVAVFVVCWPIHIVIKALITPETTQVSMHCIALGYNSCLNP
LYAFLDENFKRCFRFCIPSTISIEQNSTVRONTREHPSANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 330 a 434 c 312 g 325 t

ORIGIN

Query Match 2.9%; Score 47; DB 12; Length 1401;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
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DB 464 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 510
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RESULT 37
RNU02083 1448 bp mRNA ROD 20-JUL-1995
LOCUS Rattus norvegicus mu-opioid receptor mRNA, complete cds.
DEFINITION Rattus norvegicus mu-opioid receptor mRNA, complete cds.
ACCESSION U02083
VERSION U02083.1 GI:403573
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1448)
Bunzow, J.R., Zhang, G., Bouvier, C., Saez, C., Ronnekleiv, O.K.,
Kelly, M.J. and Grandy, D.K.
Characterization and distribution of a cloned rat mu-opioid
receptor
J. Neurochem. 64 (1), 14-24 (1995)
95096825
2 (bases 1 to 1448)
Bunzow, J.R.
Direct Submission
Submitted (24-SEP-1993) James R. Bunzow, VIABR, Oregon Health
Sciences University, 3181 S.W. Sam Jackson Park Rd., Portland, OR
97201 USA
Location/Qualifiers
1. 1448
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
211. 1407
/codon_start=1
/product="mu-opioid receptor"
/protein_id="AA170049.1"
/db_xref="GI:403574"
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TNIYIFNLADALATSTLPQSVNYLMGTPFGTILCKIVISIDYNNKFSITLCT
MSVDRIYAVCHPVKALDFRTPRNKIVNVCNMISSAIGLPMFMATTKRQSGIDCT
LTFSPHTWENLKLICVETFAFIMPLVILITVCGMLRLKSVRMATSGSKEDNRL
RITRMVLVVAVFVVCWPIHIVIKALITPETTQVSMHCIALGYNSCLNP
LYAFLDENFKRCFRFCIPSTISIEQNSTVRONTREHPSANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 345 a 443 c 326 g 334 t

Query Match 2.9%; Score 47; DB 12; Length 1448;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
|||||
DB 505 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 551
|||||

RESULT 38
RATMORA 1586 bp mRNA ROD 04-AUG-1993
LOCUS Rattus norvegicus mu opioid receptor mRNA, complete cds.
DEFINITION Rattus norvegicus mu opioid receptor mRNA, complete cds.
ACCESSION L13069

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	FEATURES
LI3069.1	GI:348250	mu opioid receptor.	Rattus norvegicus	Whole brain cDNA to mRNA.					
1	(bases 1 to 1586)								
Chen, Y., Mestek, A., Liu, J., Hurley, J. A. and Yu, L.									
Molecular cloning and functional expression of a mu-opioid receptor									
from rat brain									
Mol. Pharmacol. 44, 8-12 (1993)									
93341493									
Location/Qualifiers									
1..1586									
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210..1406									
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/translation="MDSSTGPGNTSDCSDP1AQAQSCSPAPGSPWLNLSHVDGNQSDPGCG									
LNRGLGNDSLCPQGTGSPSWNTATITMALYSIYCVGLFENFLVMYVIVYTKMTKTA									
TNIVIFNLADALATSLPQOSVNYLGMWPGTICKIVISIDYNNFISPTLCT									
MSVBYIAVCHPVKALDRPRNAKIVVCAWIISSAIGLPVMEATTKYRQSIDCT									
LTFEHPYMWENLTKICVFATFIMPLIITIVCGGLMLRKSVRMSGSKENRNLRI									
RITRVLVYVAVFTVCMPIHIIYIKALITIPETROTYSWFCLADGYNLSCLNFP									
LYALDENFKRFRFECIPITSSITLQONSTRVONTREHPSTANTVDRTHOLENLEEA									
ETAPLP"									
BASE COUNT	376 a	479 c	361 g	370 t					
ORIGIN									
Query Match	2.9%	Score 47	DB 12	Length 1586					
Best Local Similarity	100.0%	Pred. No. 5.4e-15							
Matches 47	Conservative 0	Mismatches 0	Indels 0	Gaps 0					
539	ATGAGAGCTGCCACCAACATCTACATTTTCACACCTGTCCTCGGCAGA	585							
Db 504	ATGAGAGCTGCCACCAACATCTACATTTTCACACCTGTCCTCGGCAGA	550							
RESULT 39									
RATMORI									
LOCUS	RATMORI	2135 bp	mRNA	ROD	21-OCT-1993				
DEFINITION	Rattus norvegicus Mu opiate receptor (MUORI) mRNA, complete cds.								
ACCESSION	L20684								
VERSION	L20684.1	GI:409149							
KEYWORDS	Mu opiate receptor.								
SOURCE	Rattus norvegicus (library: lambda ZAP (Stratagene)) cortex cDNA to								
	mRNA.								
ORGANISM	Rattus norvegicus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;								
REFERENCE	1 (bases 1 to 2135)								
AUTHORS	Wang, U.-B., Imai, Y., Epler, M. C., Gregor, P., Spivak, C. and Uhl, G. R.								
TITLE	Mu opiate receptor: cDNA cloning and expression								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234 (1993)								
MEDLINE	94052137								
FEATURES	Location/Qualifiers								
source	1..2135								
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	31..1227								
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CDS	31..1227								

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/protein_id="AAA1643.1"
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MSVDRYIACVHPKALDFERTPRNAKIVNVCNWLSSAIGLPVFMATYTKRQSDIDCT
LTSHPYMWENMLKICVFIFAFIMPLYLITVCGLMILRLKSVRMKSGSKEDNRLR
RITFMVAVVAVFICWTPPIHIVYIIKALITITETPQTSMHFCIALGTNSCLNPV
LYALFDENFRKFRFCPIPTSIITSEQDNSTRVQNTREHSTANTYDRTNHOJLENLA
ETAPLP"
BASE COUNT      541 a      590 c      441 g      563 t
ORIGIN
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Query Match      2.9%; Score 47; DB 12; Length 2135;
Best Local Similarity 100.0%; Pred. No. 5,4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      539 ATGAGACTGCCACCAACATCTACATTTTCAACCTGCTCGCAGAG 585
      |||||||
DB      325 ATGAGACTGCCACCAACATCTACATTTTCAACCTGCTCGCAGAG 371
      |||||||

RESULT 40
RATROB      2397 bp      mRNA      ROD      04-FEB-1999
LOCUS      Rat mRNA for rat opioid receptor B, complete cds.
DEFINITION      D16349
ACCESSION      D16349.1
VERSION      GI:391866
KEYWORDS      G-protein coupled receptor; rat opioid receptors; transmembrane
      protein.
SOURCE      Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
      PROR15.
ORGANISM      Rattus norvegicus
      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
      Rodentia; Scurionath; Muridae; Murinae; Rattus.
REFERENCE      Takeshima, H.
      Title      Direct Submission
      Author(s)      Submitted (03-JUN-1993) to the DDBJ/EMBL/Genbank databases. Hiroshi
      Journal      Takeshima, International Institute for Advanced Studies; C/O
      Title      Shimadzu Corporation N-80, 1 Nishinokyo-Kuawahara-cho, Kyoto 604,
      Reference      Japan (Tel:075-823-1208, Fax:075-811-8186)
      Authors      2 (bases 1 to 2397)
      Title      Fukuda, K., Kato, S., Mori, K., Nishi, M. and Takeshima, H.
      Reference      Primary structures and expression from cDNAs of rat opioid receptor
      Authors      delta- and mu-subtypes
      Title      FEBS Lett. 327 (3), 311-314 (1993)
      Reference      93351652
      Title      Submitted (03-JUN-1993) to DDBJ by:
      Authors      Hiroshi Takeshima
      Title      International Institute for
      Reference      Advanced Studies
      Authors      C/O Shimadzu Corporation N-80
      Title      1 Nishinokyo-Kuawahara-cho
      Reference      Kyoto 604
      Authors      Japan
      Title      Phone: 075-823-1208
      Reference      Fax: 075-811-8186.
      Authors      Location/Qualifiers
      Title      1. 2397
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      Authors      /strain="Wistar"
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      Reference      /dev_stage="adult"
      Authors      /tissue_type="brain"
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      Reference      /gene="ROR-B"

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MSYDRYAVCHPKALDEPRIPRNKIVNCONMILSSAIGLPMVMATTKYRQSDICT
LTSPHPTWENELTKICVFIFAPMLVITTCGMLTKLSYRMSSKREDRNR
RTRRMVLVAVFIVCTPPIHIYIKALITTPETRTQTSMEPCIALGTTNSCLNRY
LVAFDENFRFCFECIPISSTLEQNSRVRONTREHPSSTANTYDRINHOLENLEA
ETAPLP"
BASE COUNT      614 a      650 c      506 g      627 t
ORIGIN

Query Match      2.98; Score 47; DB 12; Length 2397;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
Db 478 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 524

RESULT 41
LOCUS      S77863      720 bp      mRNA      ROD      26-SEP-1995
DEFINITION mu-opioid receptor MOR [rats, peritoneal macrophages, mRNA Partial,
720 nt].
ACCESSION  S77863
VERSION     S77863.1 GI:998526
KEYWORDS
SOURCE      Rattus sp. peritoneal macrophages.
ORGANISM    Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 720)
            Sedqj.M., Roy,S., Ramakrishnan,S., Elde,R. and Loh,H.H.
            Complementary DNA Cloning of a mu-opioid receptor from rat
            peritoneal macrophages
            Biochem. Biophys. Res. Commun. 209 (2), 563-574 (1995)
JOURNAL    MEDLINE
MEDLINE    95251654
REMARK     Genbank staff at the National Library of Medicine created this
            entry [NCBI gidsq 166498] from the original journal article.
            This sequence comes from Fig. 3.
FEATURES
            source
            1..720
                Location/Qualifiers
                /organism="Rattus sp."
                /db_xref="taxon:10118"
                1..720
                /partial
                /gene="mu-opioid receptor MOR"
BASE COUNT      168 a      221 c      144 g      187 t
ORIGIN

Query Match      2.58; Score 41; DB 12; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 545 ACTGCACCAACATCTACATTTTCAACCTGCTGGCAGA 585
Db 1 ACTGCACCAACATCTACATTTTCAACCTGCTGGCAGA 41

RESULT 42
LOCUS      CPUG7928      354 bp      DNA      ROD      02-JAN-1997
DEFINITION Cavia porcellus mu-opioid receptor gene, partial cds.
ACCESSION  U67928
VERSION     U67928.1 GI:1763012

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KEYWORDS
SOURCE      domestic guinea pig.
ORGANISM    Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
REFERENCE   1 (bases 1 to 354)
            Ronnkleiv,O.K., Bosch,M.A., Cunningham,M.J., Wagner,E.J.,
            Grandy,D.K. and Kelly,M.J.
            Down regulation of mu-opioid receptor mRNA in the medbasal
            hypothalamus of the female guinea pig following morphine treatment
            Unpublished
JOURNAL     2 (bases 1 to 354)
AUTHORS     Grandy,D.K.
TITLE       Direct Submission
JOURNAL     Submitted (25-AUG-1996) Vollum Institute, 3181 S.W. Sam Jackson
            Park Rd., Portland, OR 97201, USA
FEATURES
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                /db_xref="taxon:10141"
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                /number=1
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                /product="mu-opioid receptor"
                /protein_id="FAB39617.1"
                /db_xref="GI:1763013"
                /translation="YTKMKATNIIYFNALADALATSTLPGSVNLMGTRFECITL
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                76..152
                /note="encodes transmembrane domain II"
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BASE COUNT      91 a      98 c      60 g      105 t
ORIGIN

Query Match      2.48; Score 38; DB 12; Length 354;
Best Local Similarity 100.0%; Pred. No. 7.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 ATCTACATTTTCAACCTGCTGGCAGATGCCCTTAC 594
Db 88 ATCTACATTTTCAACCTGCTGGCAGATGCCCTTAC 125

RESULT 43
LOCUS      S79903      1944 bp      DNA      ROD      17-FEB-1996
DEFINITION mu opioid receptor [exon 1, promoter] [rats, Genomic, 1944 nt].
ACCESSION  S79903
VERSION     S79903.1 GI:119532
KEYWORDS
SOURCE      Rattus sp.
ORGANISM    Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 1944)
            Kraus,J., Horn,G., Zimprich,A., Simon,T., Mayer,P. and Holt,V.
            Molecular cloning and functional analysis of the rat mu opioid
            receptor gene promoter
            Biochem. Biophys. Res. Commun. 215 (2), 591-597 (1995)
JOURNAL    MEDLINE
MEDLINE    96011819
REMARK     Genbank staff at the National Library of Medicine created this
            entry [NCBI gidsq 172339] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES
            source
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mRNA 1361. >1944
gene 1661. 1944

BASE COUNT 498 a 468 c 446 g 532 t
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Query Match 2.28; Score 35; DB 12; Length 1944;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 CTCTCGAAGTCTCCGTCATGATGATGATGT 525
Db 1907 CTCTCGAAGTCTCCGTCATGATGATGATGT 1941

Search completed: November 14, 2000, 23:48:26
Job time: 7524 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 22:43:22 ; Search time 86.83 Seconds
(without alignments)
6965.529 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGACCCTCTGTAAGT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: OLIGO_MUC
Gapop 60.0 , Gapext 60.0

Searched: 480022 seqs, 187831343 residues

Word size : 35

Total number of hits satisfying chosen parameters: 33

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1610	100.0	1610	16	089226 Human mu oploid re
2	1256	78.0	2162	19	V61984 Human mu-oploid re
3	1256	78.0	2162	19	V61995 Human mu-oploid re
4	1240	77.0	2160	16	Q93102 Human mu opiate re
5	1240	77.0	2162	21	288470 Human mu oploid re
6	1215	75.5	2162	19	V61985 Human mu-oploid re
7	1205	74.8	2162	19	V61986 Human mu-oploid re
8	1205	74.8	2162	19	V61987 Human mu-oploid re
9	1205	74.8	2162	19	V61988 Human mu-oploid re
10	1205	74.8	2162	19	V61989 Human mu-oploid re
11	1205	74.8	2162	19	V61990 Human mu-oploid re
12	1205	74.8	2162	19	V61991 Human mu-oploid re

13	1205	74.8	2162	19	V61992 Human mu-oploid re
14	1205	74.8	2162	19	V61993 Human mu-oploid re
15	1205	74.8	2162	19	V61994 Human mu-oploid re
16	441	27.4	441	20	X59781 DNA encoding a mu3
17	392	24.3	829	15	Q56703 Partial sequence o
18	59	3.7	268	21	260733 Murine mu-oploid r
19	59	3.7	1238	21	260727 CDNA encoding mur
20	59	3.7	1257	21	260730 CDNA encoding mur
21	59	3.7	1334	21	260728 CDNA encoding mur
22	59	3.7	1346	21	260737 CDNA encoding mur
23	59	3.7	1365	21	260736 CDNA encoding mur
24	59	3.7	1423	21	260726 CDNA encoding mur
25	59	3.7	1542	21	260729 CDNA encoding mur
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27	59	3.7	1729	21	260734 CDNA encoding mur
28	59	3.7	1981	15	Q56705 Partial sequence o
29	59	3.7	2045	21	260735 CDNA encoding mur
30	59	3.7	2229	19	V49252 Mouse mu opiate re
31	47	2.9	1618	16	089222 Rat mu oploid rece
32	47	2.9	1618	16	089223 Transcription regu
33	47	2.9	2070	15	Q79199 Rat mu-subtype op

ALIGNMENTS

RESULT 1

Q89226 ID Q89226 standard; CDNA; 1610 BP.

XX Q89226;

DT 20-OCT-1995 (first entry)

XX Human mu oploid receptor CDNA.

DE Human mu oploid receptor; MOR; gene therapy; diagnostic; ss.

XX Mu oploid receptor; MOR; gene therapy; diagnostic; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 239..1441

FT /tag= a

PN W09507983-A.

XX 23-MAR-1995.

PD 13-SEP-1994; 34WO-US10358.

PF 13-SEP-1993; 93US-0120601.

PR (INDV) UNIV INDIANA FOUND.

PA Yu L;

XX WPI; 1995-131351/17.

DR P-PSDB; R71966.

XX New nucleic acid encoding new human mu oploid receptor - and

PT related vectors, transformed cells, antibodies etc., useful in

PT diagnosis, treatment and drug screening.

XX Claim 5; Page 208-210; 266pp; English.

XX A CDNA library constructed from human caudate nucleus mRNA was

CC screened with rat mu oploid receptor CDNA under conditions of

CC low stringency. One positive clone included the sequence given in

CC Q89226, encoding a mu oploid receptor MOR (R71964). The CDNA

CC is used for prodn. of recombinant MOR, in gene therapy, etc.

XX Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

SO

Query Match 100.0%; Score 1610; DB 16; Length 1610;
 Best Local Similarity 100.0%; Pred. No. 0;
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D 1 cggatgagctctgtgaagtgaggagggtctatagcagagagaaatgtcag 60
QY 61 ATGCTAGCTCGGTCCTCCGCTGACGCTCTCTGTCTCAGCAGAGACTGTTCT 120
D 61 atgctagctcggtcctccgctgacgctctctgtctcagcagagactgttct 120
QY 121 GTAAGAAGACAGAGAGCTGTGCGAGCGGCGAAAGAGAGCGGCTTGAACCC 180
D 121 gtaagaagacagagagctgtgcgagcgaggaaagagcggtcggttgaaacc 180
QY 181 GAAAAGTCTGGTGTCTGCTGCTACCTGCGACAGCGTCCCGCGGCGCTGATACAT 240
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QY 241 GGACAGAGAGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
D 241 ggacagagagctgtgcgggcgggcgggcgggcgggcgggcgggcgggcgggcg 300
QY 301 TTGCTCCCGACAGACCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
D 301 ttgctcccgacagacccgcggtctgctgctgctgctgctgctgctgctgctgctg 360
QY 361 GTCCGACCATGCGGCTCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
D 361 gtccgaccatgctgctcgagacggcgggcgggcgggcgggcgggcgggcgggcg 420
QY 421 GACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
D 421 gaccggagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 480
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D 481 cgtgtgggctcttcgaaacttcgtgctgctgctgctgctgctgctgctgctgctg 540
QY 541 GAAGACTGCCACCAACATCTACATTTTCAACCTTCTGCTGCGAGATCCCTTACCCAC 600
D 541 gaagactgccaccaacatctacatTTTTCAACCTTCTGCTGCGAGATCCCTTACCCAC 600
QY 601 TACCGTCCCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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D 661 ttgcaagatagTATCTCCATAGATTAATACATGTTGACACGATATTCACCTCTG 720
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QY 841 TCTTCTGTATGTTGATGCTACACAAATACAGGAGGTTCCATAGATTGACACT 900
D 841 tctTCTGTATGTTGATGCTACACAAATACAGGAGGTTCCATAGATTGACACT 900
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D 901 aacATTTCTCATCAACCTGCTGTAAGTCTGCTGTAAGTCTGCTGTAAGTCTGCTG 960
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QY 1021 CAAGAGTGTCCGATGCTCTGTGCTCCAAAGAAAAGACGAGAAATCTTGAAGATAC 1080
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D 1081 caggatgTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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D 1141 cgTCATATTAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
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D 1321 gcaACAAACTCCATCTGATTTGCTGAGACACTAGAGACACCCCTCCAGGCGCAATAC 1380
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D 1441 acaAGGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
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D 1501 agGTGCTTCAAGAAATGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
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RESULT 2
ID V61984
XX V61984 standard; cDNA; 2162 BP.
XX
AC V61984:
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW predisposition; addiction; analgesic; anesthetic; anti-addictive;
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT misc_feature 502..503
FT /tag= b
FT misc_feature 855..856
FT /tag= c
FT /note= "Site of intron 1"
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PN W09833937-A2.

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AC	XX	11-DEC-1995 (first entry)			
DT	XX	Human mu opiate receptor cDNA.			
DE	XX	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;			
KW	XX	drug abuse; analgesic; ds.			
OS	XX	Homo sapiens.			
XX	XX	Key Location/Qualifiers			
FH	FT	CDS 213..1415			
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XX	XX	W09520667-A1.			
PN	XX	03-AUG-1995.			
PD	XX	30-JAN-1995; 95MO-US01144.			
PE	XX	28-JAN-1994; 94US-0188275.			
PR	XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.			
PA	XX	(USSH) US SEC DEPT HEALTH.			
XX	XX				

PI Johnson PS, Persico AM, Uhl G, Wang J;
XX
XX WPI: 1995-275452/36.
DR P-PSDB; R/6780.
XX
XX New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PT
XX
XX Claim 4; Page 24-25; 49pp; English.
XX
XX hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR
CC DNA can be used as probes to examine the structure and function of
CC hMOR genes or to screen individuals for susceptibility to drug
CC abuse. Expression in e.g. COS cells allows production of
CC recombinant hMOR.
XX
XX Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T; 0 other;

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OY	343	CCACTTAATATGCAACCTGTCCGACCCATGTGGGTGCCAACCAGCACGACTGGCGGAG	402	
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OY	403	AGACAGCTGTGGCCTCGACGGGAGTCCCATGTATGACGGGCATCAGATATGGC	462	
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OY	523	TGTCAATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACTTGGCTTGGC	582	
Db	497	tgctcagatcacccaagatgaagactgtccacaacatctacacttccaactctgtcctggc	556	
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OY	643	GCCATTTGGAACCATCTTTTGCAAGATAGTATCTCCATTAATTACTTAAACATGTTAC	702	
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OY	703	CAGCATATTCAACCTCTGTACACATGATGATGTGATGATACATTGCACTGTGCCACCTGT	762	
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Db 1397 aactgctcgtgttcacctaacagggtctcatgcatcctcgaacttccaaagcttagaagc 1456
QY 1483 CACCATGTATGTGGAAGCAGGTGCTTCAAGAAATGTAGAGGCTCTTAATTTCTTAGGA 1542
Db 1457 caccatgattgtggaagcaaggttgcttcaagaatgtgtagaagagctctaattctcaga 1516
QY 1543 AAGTGCCTGCTTTTGAAGCATCACTCACTCTTCTCTGAGGCACTGCTGCTGACACT 1602
Db 1517 aatgacctactttatgcatcaccacaccttccctctcctgacctgctcctgacact 1576
QY 1603 AGAGG 1607
Db 1577 agagg 1581

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RESULT 5
ID 288470
ID 288470 standard; DNA; 2162 BP.
AC 288470:
XX
XX 11-MAY-2000 (first entry)
XX
XX Human mu opioid receptor gene.
DE
XX Human mu opioid receptor: hMOR1; diagnosis: addiction; constipation;
KW diarrhoea; decreased immune response; stress; gastrointestinal motility;
KW immune response; hypothalamus; pituitary; adrenal axis; gonadal axis;

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KW pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;
KW anxiolytic; alcohol; ds.
XX
OS Homo sapiens.
PN MO200003024-A2.
XX
XX 20-JAN-2000.
XX
XX 10-JUL-1999; 99MO-US15707.
XX
XX 10-JUL-1998; 98US-0113426.
PR 09-JUL-1999; 99US-0113426.
XX
PA (UYRO.) UNIV. ROCKEFELLER.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX Kreek MJ, LaForge KS, Yu L, Tischfield JA;
PI WPI: 2000-160930/14.
DR P-PSDB: Y79945.
XX
XX New human opioid mu receptor gene variant for determining
PT susceptibility of a subject to addictive disorder, pain -
XX
XX Claim 1; Page -; 134pp; English.
XX
CC The present invention describes an isolated variant (V) of the human
CC mu opioid receptor (hMOR1) gene with at least two variations A118G,
CC C117, G24A, G775A or G942A of the sequence of Genbank accession number
CC L25119. Determination of increased or decreased susceptibility in a
CC subject to at least one addictive disorder like opioid, cocaine,
CC nicotine, barbiturate or sedative hypnotic, anxiolytic, alcohol
CC addiction or addiction to others psychostimulants and to pain is done
CC by determining the presence of (V) with variation A118G or C117
CC respectively in one and/or both alleles of (V) and it can also be done
CC by determining the presence of the hMOR1 protein with variation Asn40Asp
CC or Ala6Val respectively. Therapeutically effective amount of pain
CC reliever to induce analgesia or therapeutic agent to treat one additive
CC disorder is determined by determining the variations in the hMOR1 gene
CC or protein and so increased or decreased susceptibility indicates an
CC increased or decreased amount of pain reliever or therapeutic agent
CC respectively. The determination of the hMOR1 gene with variation A118G
CC or C117 also helps in the diagnosis of a disease or disorder like
CC infertility, constipation, diarrhoea, decreased immune response or
CC decreased ability to withstand stress related to physiological function
CC like sexual or reproductive function, gastrointestinal motility, immune
CC response, or ability to withstand stress regulated by hypothalamus
CC pituitary adrenal axis (HPA) or gonadal axis (HPG). The present sequence
CC represents the hMOR1 gene.
CC N.B. The present sequence is not given in the present invention but
CC is referred to as the Genbank accession number L25119.
XX
XX Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 2 other:
SO

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Query Match 77.0%; Score 1240; DB 21; Length 2162;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 44 GCAAGAGAAATGTCAAGTCTCAGTCCCTCCCTCCGCTGACGCTCTCTGTCTC 103
Db 17 gcagagaggaatgcatcagatgctcagctccctccctccgctcgtcctctctc 76
QY 104 AGCAGACATGCTTCTGTAAGAAAGCAGAGACCTGTGACGGGGAAGGAAGGGCC 163
Db 77 agcagagactgcttctgtaagaacagcagagctgtggaagcggaaggaagagc 136
QY 164 TGAGGCGCTTGAACCCGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 222
Db 137 tgaagcgcttgaaacccgaaagctcgtgctcctcgtcctcgtcctcgtcgtgccc 196
QY 223 CCCGCGCTGATGACATGACAGACGCGCTGCCCAAGCAAGCCAGCAATTGCTACTGA 282

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Db 197 cccgcccagctacagcatgagacagcagcgtgccccacagcaagccagcaattgcaactga 256
QY 283 TGGCTTGGGCTACTCAAGTTGCTCCCGACAGCCAGCCCGGTTCTGGGTCAACTTGTGTC 342
Db 257 tgccttggcgtactcaagtgtctcccaagaccagcccggttctcgtgggtcaactgttc 316
QY 343 CCATTAGATGGAGACCTGTCCGACCATGGGTCCGAACCGACGCACTGGGGGAG 402
Db 317 ccaacttagatgagcaacctgtccgacccaatgcygtccgaacccgacccaacctggcg99ag 376
QY 403 AGACAGCTGTGCTCCGACCGGAGTCCCTCATGATGATCAGGCGCATCAGATCATGCG 462
Db 377 agcagcgcgtgtccctccgacgagccctccctcaatgatacgccatccagatcagc 436
QY 463 CCTCTACTCATGTGTGCGTGGTGGGCGCTTTGGGAACTCTCTGGTCAATGTATGTAT 522
Db 437 cctctactccatcgtgtgcygtgggtgggctcttcggaactctcgtgtcatgtatgtat 496
QY 523 TGTGAGATACCAAGATGAGAGTGGACATGACCAACATCTACTATTTCACCTGTCTGGC 582
Db 497 tgcagatacaacaagaatgagacgtcccaacaacatcattcaccctgtcctg9c 556
QY 583 AGATGCTTAGCCACAGTACCTGCTTCAGAGTGTGATTTACCTAATGGGAAATG 642
Db 557 agatgctctagccaccagatccctgtccctccagagtgatgatacttaattggaaatg 616
QY 643 GCCATTGGACACATCCTTTGCAAGATAGTATCTCATATGATTACTATATACATGTTTAC 702
Db 617 gccatttggacacatccttggcaagatagatgtccatcattacatacaatgttcac 676
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Db 677 cagcattacacccctcgtccacatgagctgtgatacgaatactgcaatccgcaacctgt 736
QY 763 CAAGGCTTAGATTTCCGCTACTCCCGAAATGCCAAATATATCATATGTCGCAACTGGAT 822
Db 737 caagccttagatcttcgctaccccgaaatgcaaaattcaatgctcgaactgtat 796
QY 823 CCTCTCTTACGCAATGCTTCTCTGTATGTTGATGCTGATGATGATGATGATGATGATG 882
Db 797 cctctcttccagcatgtgtctctgttaatgttcatgtgcacaaacaaatatacagcaag 856
QY 883 TTCCATAGATGTACACTAATCTCTCATCAACCTGTACTGGGAAACCTGCTGAA 942
Db 857 tcccatagatgtgacacatacattctcaccacacccgtgactg99aaaccccg9aa 916
QY 943 GATCTGTGTTTTCATCTTCCCTTCAATATGACAGTGTCTCATTAACCTGTGCTATG 1002
Db 917 gatctgtgtttcatcttgcctctcattatgacagtgctcattacatcagtgctatg 976
QY 1003 ACTGATGATCTTCCGCTCAAGAGTGTCCGATGCTCTCTGCTCCAAAGAAAGACAG 1062
Db 977 actgatgatcttgcgctcagaagatgctcgaatgtctcgtctccaaagaagaagacag 1036
QY 1063 GAATCTTCGAAGATACCGAGATGCTGTGATGCTGTGCTGTGCTGTGCTGTGCTGTG 1122
Db 1037 gaactctggaagatcacccagatgtgctg9gtg9gtg9gtg9gtg9gtg9gtg9gtg9 1096
QY 1123 GACTGCCATTGACATTTACGTATCAATTAAGCCTTGTTTACAATCCAGAACTAGCT 1182
Db 1097 gactcccatcattacattacgtcattacaaagccttggttaacaatcccaagaactagct 1156
QY 1183 CCAGATGTTTCTTGGACATCTTGCATGTGCTAGTTTACAAACAGCTGCTCAACCC 1242
Db 1157 ccagactgttcttgcacttgcactgtcctcaggttatacaaaagcgtcgtcacaacc 1216
QY 1243 AGTCTTTATGATTTCTGTGATGAAACTCAACGATGCTTCAAGAGTGTCTGTATCC 1302
Db 1217 agtctttaaagcttctcgtatgaaacatcacaagatgtctcagagagttctgtatccc 1276
QY 1303 AACCTCTTCCAACTTGAAGCAACAAACTCCACTGCAATTCGTAGAACTAGAGACCA 1362

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Db 1277 aacctctccaaattgagcaacaacacccactgaaattcgtcagaaactagagacca 1336
QY 1363 CCCCTCCAGGGCAATACAGTGGATGAACTATATCTACGTAGAAAACTTGGAAACACA 1422
Db 1337 cccctccagggccaatatacagtgatagaactaatcatcagctagaaatctg9aagcaga 1396
QY 1423 AACTGCTCGTTACCTTAACAGAGGCTCATGACATCCGACCTTCCACCAAGCTTAGAAC 1482
Db 1397 aactgtccggtgtccctcaagaaggtctcattgcattccgaccttcaacagcttagaagc 1456
QY 1483 CACCATGATATGTGGAAGCAGGTGCTTCAAGATGTGTAGAGGCTCTAATTTCTTAGGA 1542
Db 1457 caccatgatatgtgaaagcaggtgtcctcaagaatgtataggaggtccttaattctcagga 1516
QY 1543 AAGTGGCTGCTTTTAAAGTATCAACCTTTTCTCTGTGCGACATCTGCTGCAAT 1602
Db 1517 aagtgctactttagtcatccaaactcttctcctcgtccacactgtcgtcacatt 1576
QY 1603 AGAGG 1607
Db 1577 agaggg 1581

RESULT 6
ID V61985
V61985 standard; cDNA: 2162 BP.
AC V61985;
DE 11-JAN-1999 (first entry)
XX
XX Human mu-opioid receptor cDNA variant 1.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX prediction; addition; analgesic; anesthetic; anti-addictive;
XX psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 213..2040
XX FT /tag= a
XX FT /product= "mu-opioid receptor"
XX FT misc_feature 502..503
XX FT /tag= b
XX FT /note= "Site of intron 1"
XX FT misc_feature 855..856
XX FT /tag= c
XX FT /note= "Site of intron 2"
XX FT misc_feature 1376..1377
XX FT /tag= d
XX FT /note= "Site of intron 3"
XX FT mutation 41
XX FT /tag= e
XX FT /note= "Wild type G is replaced by T"

PN WO9833937-A2.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-DE00382.
XX
XX 03-FEB-1997; 97DE-1003925.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Hoehe M, Wendel B;
XX
XX WPI: 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -

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KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KV	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
XX	
XX	Synthetic.
XX	
FT	Key
FT	Location/Qualifiers
FT	213..2040
FT	/tag= a
FT	/product= "mu-opioid receptor"
FT	502..503
FT	/tag= b
FT	/note= "Site of Intron 1"
FT	855..856
FT	/tag= c
FT	/note= "Site of Intron 2"
FT	1376..1377
FT	/tag= d
FT	/note= "Site of Intron 3"
FT	80
FT	/tag= e
FT	/note= "Wild type C is replaced by T"
XX	
PN	WO9833937-AZ.
XX	
PD	06-AUG-1998.
XX	
PF	02-FEB-1998; 98WO-DE00382.
XX	
XX	03-FEB-1997; 97DE-1003925.
PR	
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX	
PI	Hoehe M, Wendel B;
XX	
DR	WPI, 1998-437487/37.
XX	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -
PT	development, e.g. to predict pre-disposition to addiction and for
PT	development of analgesics, anaesthetics and anti-addiction agents
XX	
XX	
PS	Claim 8; Page -: 26pp; German.
XX	
CC	This sequence encodes a novel human mu-opioid receptor in which a C
CC	nucleotide at position 80 of the wild-type sequence represented in
CC	V61984 is replaced by a T. The wild type receptor and its variants,
CC	polymorphisms and mutants are used in a method for detecting
CC	pre-disposition to disease, particularly addictive disease, by isolating
CC	DNA from a sample, genotyping selected positions and comparing with a
CC	reference DNA. Such sequences are used to develop analgesic, anesthetic,
CC	anti-addictive and psychopharmaceutical agents, to construct genes and
CC	vectors, particularly for pharmaceutical development, to develop
CC	diagnostic kits for predicting risk of addiction, response to analgesics
CC	or anaesthetics, or development of side effects from a drug. Particular
CC	applications are to determine risk of addiction to opiates or cocaine, or
CC	of developing inherited alcoholism.
CC	Note: This sequence is not represented in the specification and has
CC	been constructed from the wild-type sequence represented in V61984 in
CC	accordance with the specification.
XX	
XX	
SO	Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;
XX	
Query Match	74.8%; Score 1205; DB 19; Length 2162;
Best Local Similarity	99.6%; Pred No. 0.
Matches 1575; Conservative	0; Mismatches 5; Indels 1; Gaps 1
QY	28 TGGAGAGGGGCTATACGCAGAGAGAGATCTCAGATCTCAGTCCGCTCCGCTCGA 87
Db	1 TGGGAGGAGGCGTACATACGCGAGAGAGATCTCAGATCTCAGTCCGCTCCGCTCGA 60
QY	CGCTCTCTCTCTCTCAGCAGAGACTGGTTTCTGTAAAGAAACAGCAGAGAGCTGTGCACG 147

Db	61	cgcccctctctgctcagcgctaggaactcgtgttctctgtaagaagaacagcaggagctcgtgacgc	120
Oy	148	ggccaaaggaaaggcgctgagagcccttggaaacccggaaatctcggctgctctgagcttacct	207
Db	121	ggcgaaagaagcgcgcctgagcgctcttggaaccggaaatctccgtgtgctctcgttacct	180
Oy	208	gcgcacac - gngccggccggccggcgtgagacatgatgacagcagccctgccccacagacg	266
Db	181	cgacagcaggtgccccgcgcgcgtctagtaacatgtaacagcagcgtcccccaagacgc	240
Oy	267	ccagcaatttgcactgattgctcttgccgtactcaattgctccccagacaccagccccggt	326
Db	241	ccagcaaatgcacatgacctgttcgtctgtaactaagttgctccccagacaccagccccggt	300
Oy	327	cctggggaacttgcttcccacttattgagtggaacactgtgcacaccatgacggctgcgaacccga	386
Db	301	ccgtgggtcaactgtccctcacttaagtggaacactgtgcgaacccatgaggtgccgaacgcga	360
Oy	387	ccgacacttgggggggagagacagcctgtgccccttcgacccggcagtcctctcatgatcagcg	446
Db	361	ccaaacctggcgaggagagacagcctgtgcctccgcagcgcagtcctcccatgatcacgcg	420
Oy	447	ccatcagagatcagagccctctactccatcgtgtgctgtggggctcttggaaactcc	506
Db	421	ccatcagagatcagagccctctactccatcgtgtgctgtggggctcttggaaactcc	480
Oy	507	tggatcatgtagtgatgtgtagatgagatgacacagatgagaactccacacaaatctcattt	566
Db	481	tggtcatgtagtgatgtgtagatgagatgacacagatgagaactccacacaaatctcattt	540
Oy	567	tcaaaccttgctcttgccagatgaccttggacacacagatgacctgccccttcgaagtgatg	626
Db	541	tcaaaccttgctcttgccagatgaccttggacacacagatgacctgccccttcgaagtgatg	600
Oy	627	accgaatgagggaacatggcccttgggaacacatccttggcaagtactgatacttcacatg	686
Db	601	accgaatgagggaacatggtccatttgggaacacatccttggcaagtgatgatacttcacatg	660
Oy	667	actataacatggttaccacgacatattgaccccttgcacacatgagtgatgacatgattg	746
Db	661	actataacatggttaccacgacatattgaccccttgcacacatgagtgatgacatgattg	720
Oy	747	cagatctgcgcacccgttcgaagcccttggatttgcgactcctccgaaatgcgaatattatca	806
Db	721	cagatctgcgcacccgttcgaagcccttggatttgcgactcctccgaaatgcgaatattatca	780
Oy	807	atgctctgcacactggatcctcttcttgcacacattgcttctccttaattggttaccgtacaa	866
Db	781	atgctctgcacactggatcctctctctctcagccattgcttctcgttaattgtaatggtacaa	840
Oy	867	caaaatcacagsgcaaggttccatagattgtnacatattctctatccaaccttgatct	926
Db	841	caaaatcacagsgcaaggttccatagattgtaactaactaactctctatccaaccttgatct	900
Oy	927	gggaaaaactgcgaacatgctgtgttttatctgcgccttcttattatggcagagtcacatca	986
Db	901	gggaaaaactgcggaagatctgttltcaatcttgctctcaatgacagtgctcaca	960
Oy	987	ttaccgtgtgctatgacatgattgcttggccctcagaagtgccgactcctctgct	1046
Db	961	ttaccgtgtgctatgacatgattgcttggccctcagaagtgctcgaactgctctgct	1020
Oy	1047	ccaaagaaaaagcaggaatcttgcgaagatccacagagatggtgtggggggggcgctg	1106
Db	1021	ccaaagaaaaagcaggaatcttgcgaagatccacagagatggtgtggggggggcgctg	1080
Oy	1107	tggttcatcgtctgctgacactccatttcacattttagctatcattttaaacccttgattaca	1166
Db	1081	tggttcatcgtctgctgacactccatttcacattttagctatcattttaaagccttgattaca	1140
Oy	1167	tcccgaaacactgattccacacgcttcttgcacatcccttgcacatcccttgcacatcccttgcacac	1226
Db	1141	tcccgaaacactgattccacacgcttcttgcacatcccttgcacatcccttgcacatcccttgcacac	1200

OY 1227 ACAGCTGCTCAACCCAGCTCTTATGATTTCTGGATGAAGAACTCAACGATGCTTCA 1286
 DB 1201 acaagctgctcaacccagctcttatagtatcttgaaactcaaacgtagcttca 1260
 OY 1287 GAGAGTCTGTATCCCACTCTTCCATTCATGAGCAACAAATCCATCGAATTCGTC 1346
 DB 1261 gagagctctgtatcccaactcttccaaatgagcaaaaaaccctcgaattcgctc 1320
 OY 1347 AGACACTAGAGACACCCCTCCACGGCCATATAGTGGATGAATTAATCATCATGCTAG 1406
 DB 1321 agaaactagagacacccctccacgccaatagtagtaactaatacatcagctag 1380
 OY 1407 AAAATCTGGAACGACAAACTGCTCGTTGCCCTACAGGGTCCATGCGCATCCGACCTT 1466
 DB 1381 aaaacttggaacgaaactgctcgccttgcccaagaggtctcagccatccgaacct 1440
 OY 1467 CACCAAGCTTAGAGCCACCATGTATGTGGAAGCAGTTGCTTCAAGATGTGTAGAGG 1526
 DB 1441 caccagaacttagaagcaccatgtagtggaagcaggtgctcgaagtgtgtaggag 1500
 OY 1527 CTCTAATTCCTAGAGAAAGTGGCTTTAGGTCATCCAACTCTTCTCTGCGCA 1586
 DB 1501 ctctaattctcagaagaagtgcctactttagatcatccaacctcttctcctgagcca 1560
 OY 1587 CTCTGCTGCACATTAGAGG 1607
 DB 1561 ctctgctctgcacattagagg 1581

RESULT 8

V61987
 ID V61987 standard; cDNA; 2162 BP.

AC V61987;

DT 11-JAN-1999 (first entry)

XX Human mu-opioid receptor cDNA variant 3.

XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predilection; addiction; analgesic; anesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX

XX Key Location/Qualifiers

FT CDS 213..2040 /tag- a /product- "mu-opioid receptor"

FT misc_feature 502..503 /tag- b

FT misc_feature /note- "Site of intron 1"

FT misc_feature 855..856 /tag- d

FT misc_feature 1376..1377 /note- "Site of intron 2"

FT mutation 102 /tag- e /note- "Site of intron 3"

FT mutation /note- "Wild type C is replaced by T"

XX WO9833937-A2.

XX 06-AUG-1998.

XX 02-FEB-1998; 98WO-DE00382.

XX 03-FEB-1997; 97DE-1003925.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Hoehe M, Wendel B;

XX WPI; 1998-437487/37.

PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -; 26pp; German.

CC This sequence encodes a novel human mu-opioid receptor in which a C
 CC nucleotide at position 102 of the wild-type sequence represented in
 CC V61984 is replaced by a T. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anesthetic,
 CC anti-addictive and psychopharmaceutical agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX

S0 Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 74.8%; Score 1205; DB 19; Length 2162;

Best Local Similarity 99.6%; Pred. No. 0; Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 28 TGGAGGGGGCTATACGACAGAGAAATGCATGCTCACTGCTCCCTCGCCTGA 87
 DB 1 tggagaggggggtatacagagagagagatgtagtgcagctggtccctccgctga 60
 OY 88 CGCTCTCTCTGTCTACGACGAGACTGTTTCTGTAGAAACACAGAGAGCTGTGGCAGC 147
 DB 61 cgtctctctctgtctcagccagagactgtttcttgaagaatacagagagctgtggcagc 120
 OY 148 GGGGAAAGGAAGCGGCTGAGGCGCTTGGAAACCCAAAAGTGTGGTGTCTGCTGCTACT 207
 DB 121 ggcgaagaagagcgcgtagggcgcttggaacccgaaagcttcggtctctgtactact 180
 OY 208 GGCACAGC-GTGGCCGCGCCGCGCTCAGTACATGACAGCAGCGCTGCCCCACGAGACG 266
 DB 181 ggcacagcagtggtcccgccgctcagtagtaccagtagcagcagcgtgccccacgagacg 240
 OY 267 CCAGCAATTCAGTATGATGCTTGGCGTACTAATTTGCTCCCGACAGACCCCGGTT 326
 DB 241 ccagcaattcagcagtagcttggcgtactcaagttctcccccagcaccgcccgggtt 300
 OY 327 CCTGGGTCAACTTGGCCACTTATGATGGCAACCTGTCCGACCACTGGGCTCGGACGCA 386
 DB 301 cctgggtcaacttgcacacttagatggaacccgtccgacccatggtgtcgaacgca 360
 OY 387 CCGACCTGGGGGAGAGACAGCCTGTGCCCTCCGACCGGAGTCCCTCATGTATCAGG 446
 DB 361 ccaacctgggggagagagacagcctgtgacctcgcagccgagcgtcccatcgtatcagc 420
 OY 447 CCATCAGATATAGCCCTCTACTCCATCGTGTGCTGTGGGCTCTTGGGAACTTCC 506
 DB 421 ccatacagatcatggtccctcactcactcgtgtggtgtgtgtgtgtgtgtgtgtgtgt 480
 OY 507 TGGTATGTATGTATGTGTGATGATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
 DB 481 tggatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 540
 OY 567 TCAACTTGTCTGTGACAGATGCTTAGCCACAGTACCTGCTCCCTTCCAGAGTGTGAT 625

Db	541	tcaacctgtctcttgagcagatgaccttagccaccagtagtacccttgcccttcagagtgagatt	600
Qy	627	ACCTAAATGGGAACATGGCCATTGGGAACCATCTTTGGCAAGATAGTGAATCTCCATAGATT	686
Db	601	accctaaatgggaacatgagccatttggaaacctctcttggcaagaatagatctccatagatt	660
Qy	687	ACTTAAACATNTTACACAGATATATACCCCTTGCCACCATAGATGTTGATGCATGCATATG	746
Db	661	actatacaatglttaccagcatatctcaacctctgcacacatgagtggtgtgatatacatg	720
Qy	747	CAGTCTGCCACCCCTGTCAAGGCGCTTAGATTTCGTACTCCCGCAAAATGGCAAAATTATCA	806
Db	721	cagtcgtccaccctgtcaagagccttagattcttcgtaactcccggaatgcaaaattatca	780
Qy	807	ATGTCCTGCACACTGGATCTCTCTTCAGCCCATMGCTCTCTCTGTAATGTTACATGGCTACCA	866
Db	781	atgctgcnaacttgatctctctcttcagccaatggtcttcctgtaatglttcaatgagctaa	840
Qy	867	CAAAATACAGGCACAGTTCATAGATTGTACATTAACATATCTCTCATCCAACCTGGTACT	926
Db	841	caaaatacaggcaaggttccatagatgtgataactaaatctctcatccaaacctgtaact	900
Qy	927	GGGAAAACCTGCTGAGATCTGTGTTTTCATCTTCGCCCTTATATGCAATGCTCATCA	986
Db	901	gggaaaacctctgtaaaatctgtgtttcttcactcttcgccttcaatgacagagtcacata	960
Qy	987	TTACCGTGTCGTATGAGCATGATGATCTTGCGCTCAAGAGTGCAGCATGCTCTMGCT	1046
Db	961	ttaccgtgtgtatgagctgtatgattcttggcctcacaagatgttccagatgctctctgct	1020
Qy	1047	CCAAAAGAAAAGACAGGAATCTTTCGAAGATCACACAGATGATGTGCTGTGATGTCGCTG	1106
Db	1021	ccaaagaaaagacaggaatcttcogaagaatcacagagatggtgtgtgtgtgtgtgtgt	1080
Qy	1107	TGTTATCTGCTGTGTGAGACCTCCCATTCACATTAACGTACATTAAGCGCTGGTTACAA	1166
Db	1081	tgttatctgctgtgtgagactcccatccatcaatctagatccatcaaaagccttggttaca	1144
Qy	1167	TCCGAGAAACTACTCTCCAGACTGTTTCTTGCGACATCTTGATGCTCTAGGTTACACA	1226
Db	1141	tcccgaaactagcttccagagatgttctcttgacattctgcattgtctctagttacaca	1200
Qy	1227	ACAGCTGCCTCAACCCAGTCTCTTATGCAATTTGTGATGAAAACCTCAACGATGCTTCA	1286
Db	1201	acaagctgcctcaaacccagctcttatgacattcttgatgtaaaacttcaaacgaatgctta	1260
Qy	1287	GAGAGTTCTGATCCCAACCTCTTCCAACTTACAGCAACAAAACCTCAGTCGATTTGCTC	1346
Db	1261	gagagttctgatatcccaactcttccaaacttgaagcaaaacacactccactgcgaattgctc	1320
Qy	1347	AGAACACTAGAGACACCCCTCCACGGCCAAATACAGTGTAGATGAACATTAATCATAGCTAG	1406
Db	1321	agaacactagagacacccccctccacagyccaatacagtgtagtaactatacatcagctag	1380
Qy	1407	AAATTCGTGAAGCAAGAACTGCTCCGTTTGCCCTTAACAAGGTCATCATGCAATTCGACCTT	1466
Db	1381	aaaatctggaaagcagaaactgtctcgcttgccctaaaggtcttcacatgcatcttccgaact	1440
Qy	1467	CACCAAGCTTAGAGCCACACATGATGTGGAACAGAGTTGCTTCAAGATGTGTAGAGAG	1526
Db	1441	caccaagcttagaagccaccatgtaigtgaaagcaggttgtctcaagaatgtgtagagag	1500
Qy	1527	CTCTAAATTTCTAGGAAGTGCCTGCTTTTAGTCAATCAACTCTTTCCTCTCTGGCCA	1586
Db	1501	ctctaaatctcttagaaagatggtccactttagtgcataccaaactcttctctctctgtgcca	1560
Qy	1587	CTCTGCTCTGCACATTAAGAG 1607	
Db	1561	ctctgtctctgcacattagagag 1581	

V61988	ID	V61988 standard; CDNA; 2162 BP.
XX	AC	V61988;
XX	DT	11-JAN-1999 (first entry)
XX	DE	Human mu-opioid receptor cDNA variant 4.
KM		Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM		predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM		psychopharmacological agent; diagnostic; side effect; drug; opiate;
KM		cocaine; inherited alcoholism; human; ss.
OS		Homo sapiens.
OS		Synthetic.
FH	Key	Location/Qualifiers
FT	CDS	213..2040
FT		/tag= a
FT		/product= "mu-opioid receptor"
FT		502..503
FT		/tag= b
FT	misc-feature	/note= "Site of intron 1"
FT		855..856
FT		/tag= c
FT	misc-feature	/note= "Site of intron 2"
FT		1376..1377
FT		/tag= d
FT	misc-feature	/note= "Site of intron 3"
FT		175
FT		/tag= e
FT	mutation	/note= "Wild type C is replaced by A"
XX		
PN		W09833937-A2.
XX		
XX		06-AUG-1998.
XX		
PF	02-FEB-1998;	98MO-DE00382.
PR	03-FEB-1997;	97DE-1003925.
PA	(DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.	
PI	Hoehe M, Wendel B;	
XX		
DR	WPI; 1998-437487/37.	
PS	Claim 8; Page -; 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor in which a C nucleotide at position 175 of the wild-type sequence represented in V61984 is replaced by an A. The wild type receptor and its variants, polymorphisms and mutants are used in a method for detecting predisposition to disease, particularly addictive disease, by isolating DNA from a sample, genotyping selected positions and comparing with a reference DNA. Such sequences are used to develop analgesic, anaesthetic, anti-addictive and psychopharmaceutical agents, to construct genes and vectors, particularly for pharmaceutical development, to develop diagnostic kits for predicting risk of addiction, response to analgesics or anaesthetics, or development of side effects from a drug. Particular applications are to determine risk of addiction to opiates or cocaine, or of developing inherited alcoholism.	
CC	Note: This sequence is not represented in the specification and has been constructed from the wild-type sequence represented in V61984 in accordance with the specification.	
XX	Sequence 2162 BP; 563 A; 564 G; 458 G; 575 T; 2 other;	

Query Match 74.8%; Score 1205; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0; Mismatches 5; Indels 1; Gaps 1;
 Matches 1573; Conservative 0;

28 TGGAGGGGGCTATACGAGAGAGAGATGTGATGCTCAGTCCGCTCCCTCCGCTGA 87
 1 tggaggggggctatacgagagagaatgtcatgctcagctccctccgctga 60
 88 CGCTCTCTCTGTCTCAGCAGAGAGAGCTGTTTGTGAAGAAACAGAGAGCTGTGAGAC 147
 61 cgcctctctctgtctcagcagagagactgttctgtlaagaaacagagagagctgtgacgc 120
 148 GGGGAAAGAGAGGGCTGAGGGCTTGGAAACCGAAAGCTCGGGGCTCGGGGCTACT 207
 121 ggggaaagagagagagctgagggcttggaaacccgaaagctccgggtccctgataacct 180
 208 GGCACAGC-GTGGCCCGCCCGGCGCTCAGTACCATGAGACAGAGCGCTGCCACAGAACG 266
 181 ggcacagcggtgcccgcgcgcgtcagtaacatgagacagcgctgccccacgaaagc 240
 267 CCAGCAATTCAGCTATGCTTGGCGTACTCAAGTTGCTCCCGACAGCCAGCCCGGTT 326
 241 ccagcaatctgactgactgcttgcctcaagttgctcccaagacccagcccggtt 300
 327 CCTGGGTAACCTTGTCCCACTTATGATGGCACTGTCCGACCCATGGGGTCCGAACCGCA 386
 301 cctggtaacctgtgcccaactagatggaacctgtccgaaccaatgcyggtccgaaacgcga 360
 387 CGGACCTGGGGGAGAGAGACAGCTGTGGCTCCGACCGGAGTCCCTCATGATCAGCG 446
 361 cggacctgggggagagagacagctgtggctccgacccggagtcctccatgatacagc 420
 447 CCATACGATATAGGCCCTCTACTCCATCGTGTGGTGGGGCTCTTCCGAACCTTCC 506
 421 ccatacgatataggccctctactccatcggtgtggtgggtctctcggaaacttcc 480
 507 TGGTCATGTATGTGATTGTACAGTACACCAAGATGAGAGTCCCAACATCTACATT 566
 481 tggtcattgtatgtattgtacagtacaccaagatgagagctgccaaacatctacatt 540
 567 TCAACCTTGCTGTGGAGATGCTTACGCCACAGTACCCCTGCCCTTCCAGAGTGAATT 626
 541 tcaaccttgctgtggagatgcttaccacagtaacctgcccctccagagtgtgaatt 600
 627 ACGTATGAGGAGACATGGCCATTTGGAACCATCTTTGCAAGATGATGATCCATAGATT 686
 601 acgtatgaggaacatggccatlttgaaacatcttgcagaagatgatactacatagatt 660
 687 ACTATACATGTTACACGAGATATTCACCCCTTGACACCATGATGATGATACATTG 746
 661 actataacatgttaccacgacatatacacccttgcacacatggtgtgatactatcg 720
 747 CAGTGTCCACCCCTGTCAAGGCCCTTATGATTCCTGACTCCCGAAATGCCAAATATATCA 806
 721 cagtgtccacccctgtcaagcccttagatttcgtaactcccgaaatgcaaaattata 780
 807 ATGTCTGAACGTGATCTCTTACGCCATGTGCTTCCATATGATGATGATGATCA 866
 781 atgtctgaacgtgatctcttaccgcatgtgtctcgtlaatgttcatgctgaacaa 840
 867 CAAATATACAGGCTAGGTTTCATAGATTGTACACTACATCTCTCATCCACCTGTGAT 926
 841 caaatatacaggctaggtttcatagattgtacactaacatctctcatcaacctgtact 900
 927 GGGAAACCTGCTGAAGATGTGTGTTTCATCTTGCCTTCAATATAGCAGTGTCTATCA 986
 901 gggaaacctgctgaagatgtgtgtttcatcttgccttcaatatagcaagtgctcatca 960
 987 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 961 ttaccgtgtgcatgacatgacatgacatgacatgacatgacatgacatgacatgacatgac 1020

1047 CCAAGAAAAGACAGAGATCTTCGAAGATCACAGAGATGGTGGTGGTGGCTG 1106
 1021 ccaagaaaagacagagatcttcgaagatcacagagatgggtgggtgggtgggtgggtgggt 1080
 1107 TGTTCATGCTGTGCTGAGCTCCCATTCATCAATTTACGTATCATTTAAAGCTTTGTTACAA 1166
 1081 tgttcattgctgtgctgagctcccatcattcaatgatactatcaatgatactatcaatgata 1140
 1167 TCCCAAGAACTACGTTCCAGACTGTTTCTTGGCACTTCTGATGATGATGATGATGATGAT 1226
 1141 tcccaagaaactacgltccagactgttcttggcacttctgacttgcattgtcctaaagttaaca 1200
 1227 ACAGCTGCTCAACCCCATCTCTTATGATTTCTGATGATGATGATGATGATGATGATGAT 1286
 1201 acagctgctcaaccccatctcttattgatttctgataagataactcaaatgatacttca 1260
 1287 GAGAGTTGTATCCCAACTCTTCCAACTTACGACCAAAACTCCACTGAAATTGCTC 1346
 1261 gagagttgtatcccaactcttccaaacttgcacatgagcaaaaaactccactcgatcgtc 1320
 1347 AGAAGCTAGAGACACCCCTCCAGGCAATACGATGATGATGATGATGATGATGATGATGAT 1406
 1321 agaagctagagacacccctccagcacaatagagatgataaactcaatcaatcagctag 1380
 1407 AAATCTGGAAGACAAACTGCTCCGTTGCCCTAACAGAGTCTCATGCTGACCTT 1466
 1381 aaatctggaagacaaactgctccggttgcctaacagaggtctcatgcatccgaactt 1440
 1467 CACCAAGCTTGAAGACCAACATGATGTGAAGACAGGTTGCTTCAAGATGTGAGAGG 1526
 1441 caccaagcttgaagaccacacatgtatgtgaagcaggttgcctcaagaatgtgtagagag 1500
 1527 CTCTAATCTCTAGGAAGTGGCTGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1586
 1501 ctctaattctctaggaagtggcttattgattaggtatcccaactcttccctccgcca 1560
 1587 CTCTGCTCTGACATTTAGAG 1607
 1561 ctctgctctgacattagag 1581

RESULT 10
 ID V61989 standard; cDNA; 2162 BP.
 XX V61989;
 AC
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 5.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW prediction; addition; analgesic; anaesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..2040
 FT /tag- a
 FT /product- "mu-opioid receptor"
 FT misc_feature 502..503
 FT /tag- b
 FT /note- "Site of Intron 1"
 FT misc_feature 855..856
 FT /tag- c
 FT /note- "Site of Intron 2"
 FT misc_feature 1376..1377
 FT /tag- d
 FT /note- "Site of Intron 3"
 FT mutation 229

QY 1527 CTCTAATCTCTAGGAAGGCTGCTTTAGTCATCCAACTCTTCTCTGAGCCA 1586
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 Db 1501 ctcaattctctaggaagagctcactttaggcataccacttctcctctgcca 1560
 QY 1587 CTCTGCTCTGCACATTTAGAG 1607
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1561 ctctcctctgcacattagag 1581
 RESULT 11
 V61990
 ID V61990 standard; cDNA: 2162 BP.
 XX
 AC V61990;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 6.
 XX
 KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KM prediagnosis; addition; analgesic; anaesthetic; anti-addictive;
 KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
 KM cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 213..2040
 FT /*tag- a
 FT /product- "mu-opioid receptor"
 FT 502..503
 FT /*tag- b
 FT /note- "Site of intron 1"
 FT 855..856
 FT /*tag- c
 FT /note- "Site of intron 2"
 FT 1376..1377
 FT /*tag- d
 FT /note- "Site of intron 3"
 FT 330
 FT mutation
 FT /*tag- e
 FT /note- "Wild type A is replaced by G"
 PN MO9833937-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PI Hoehe M, Wendel B;
 DR MPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -; 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which an A
 CC nucleotide at position 330 of the wild-type sequence represented in
 CC V61984 is replaced by a G. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
 CC anti-addictive and psychopharmacological agents, to construct genes and

CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX
 SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;
 Query Match 74.8%; Score 1205; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 28 TGGAGAGGGGCTATACGACAGAGAGAGATGCTAGCTGGTCCCTCGCCTGA 87
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 Db 1 tggagagggggtatacagagagagagatgctagctgggtccctcgctga 60
 QY 88 CGCTCCTCTCTGCTCAAGCCAGAGCTGTTCTGTAAAGAAACAGAGAGCTGGCAGC 147
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 cgcctcctctgctcagcagagagagctggtctgtaaagaaacagagagctggaagc 120
 QY 148 GCGCAAGAGAGCGGCTGAGCGCTTGAAACCCGAAAGTCTCGTCTGCTACT 207
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ggcgaagagagagcgctgagcgcttgaaacccgaaagctgctgctcctgact 180
 QY 208 GCGCAGC-GTGGCCGCCGCCGCTGAGTACATGACAGAGCGCTGCCCGCAGC 266
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 cgcacagcggtgcccgcgcgcgcgtacacacagacagcgctgcccacagc 240
 QY 267 CCAGCAATGTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 ccagcaattgactgactgactgactgactgactgactgactgactgactgactgact 300
 QY 327 CCGTGGTCACTTGTCCACTTAGATGACACCTGTCCGACCTGCGTCCGACCGCA 386
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 cctggtcaactgtccacttagatgagacctgtccgacacacagctgctcgaacgca 360
 QY 387 CCGACCTGGGCGGAGAGACAGCTGTGCTCCGACCGGAGTCCCTCCATGATACGG 446
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 ccaacctgggagagagagacagcctgtgcccctcgacagcgagctccatgtacag 420
 QY 447 CCATCAGATCATGCGCTCTACTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 ccatacagatcatgctcctcactccatgctgctgctgctgctgctgctgctgct 480
 QY 507 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 tggcatgatagtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 540
 QY 567 TCAACCTTGTCTGCGAGTGGCTTACGACCACTGCTGCTGCTGCTGCTGCTGCTGCT 626
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 tcaacctgtctgagagagccttagcacacagctgacccctccagagtgat 600
 QY 627 ACCTAATGGGAACATGCGCATTTGGAACCATCTTTCAGATGATGATGATGATGAT 686
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 accataatgggaacatgctccttagaacacacacacacacacacacacacacacac 660
 QY 687 ACTATAACATGTTACACAGATATTCACCTGTGACCATGATGTTGATGATGATGAT 746
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 actataacatgattacacagatattacacacacacacacacacacacacacacac 720
 QY 747 CAGTCTGCCACCCGTGAAGGCTTAATTTCCGTACTCCCGGAAAGCCAAATATCA 806
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 cagctgctcccccgttaagagccttagattcgtactcccgaaagccttaacatca 780
 QY 807 ATGCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 atgctgcaactgatactctctctcagcactgctcctctctctctctctctctctca 840
 QY 867 CAAATACAGGCAAGTTCCATAGATTGTACACTTAATTTCTCATCAACCTGTACT 926


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Db 841 caaatacagcgcaaggtccatagatgtacacacatctctccacccaacccggaact 900
QY 927 GGGAAACCTGCTGAGATCTGTGTTTCATCTTGGCTTCATTATGCCAGTGTCTATCA 986
Db 901 gggaaacacgtcgtgaagatctgtttcttcaccttcgccttaattatgcgaagtctcatca 960
QY 987 TTACCGGTGCTATGAGCTGATGATCTTGCGCCCAAGAGTGTCCGATGCTGCTGCT 1046
Db 961 ttacgtgtgtctatgagactgtatgtacttcgcgcccaagagtgctcgatgtctctgtgct 1020
QY 1047 CCAAGAAAGGAGACAGAAATCTTGAAGATCACCAGATGCTGCTGCTGCTGCTGCTG 1106
Db 1021 ccaagaagaagagacaggaatcttcgaagatcacagagatgctgtgtgtgtgtgtgtgt 1080
QY 1107 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1166
Db 1081 tgttcacgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
QY 1167 TCCGAGAACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226
Db 1141 tcccaagaacacgtctcgaacgtgtctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
QY 1227 ACAGCTGCTCAACCCAGCTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
Db 1201 acagctgtcccaacccagctctcttattgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 1287 GAGAGTTCTGTATCCCACTCTTCCAACTGAGCAACAACTCCACTGCTGCTGCTGCTG 1346
Db 1261 gaggtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
QY 1347 AGAAGACTAGAGACCCCTCCAGGCAATAGAGTATGATGATGATGATGATGATGATGATG 1406
Db 1321 agaagactagagacacccctccagcgcaatagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
QY 1407 AAATCTGAGAGAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1466
Db 1381 aaatctgagagagagaaactgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
QY 1467 CACCAAGCTTAGAAGCCACCATGATGATGAGAGAGAGTGTGCTTACGAATGTGTAGAGG 1526
Db 1441 caccagacttagaagcaccacatgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
QY 1527 CTGTAATCTCTAGGAAGTGGCTGCTTATGATGATGATGATGATGATGATGATGATGATG 1586
Db 1501 ctctaaatctcttagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
QY 1587 CTCTGCTCTGCACATTAGAGG 1607
Db 1561 ctctgtctgtgcacttagag 1581

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RESULT 12
V61991
ID V61991 standard; cDNA; 2162 BP.
XX
AC V61991;
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 7.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW prediagnosis; addition; analgesic; anaesthetic; anti-addictive;
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX
FH Synthetic.
FT
Key Location/Qualifiers
CDS 213..2040
FT /*tag= a

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FT misc_feature /product= "mu-opioid receptor"
FT 502..503
FT /*tag= b
FT /note= "Site of intron 1"
FT misc_feature /tag= 856
FT 855..856
FT /*tag= c
FT /note= "Site of intron 2"
FT misc_feature /tag= 1376..1377
FT 1376..1377
FT /note= "Site of intron 3"
FT mutation
FT 666
FT /*tag= e
FT /note= "Wild type A is replaced by G"
W09833937-A2.
06-AUG-1998.
02-FEB-1998; 98MO-DE0382.
PR 03-FEB-1997; 97DE-1003925.
(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
Hoehle M, Wendel B;
WPI; 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX PT used, e.g. to predict pre-disposition to addiction and for
XX PT development of analgesics, anaesthetics and anti-addiction agents
XX
XX Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX CC nucleotide at position 666 of the wild-type sequence represented in
XX CC V61984 is replaced by a G. The wild type receptor and its variants,
XX CC polymorphisms and mutants are used in a method for detecting
XX CC predisposition to disease, particularly addictive disease, by isolating
XX CC DNA from a sample, genotyping selected positions and comparing with a
XX CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX CC anti-addictive and psychopharmacological agents, to construct genes and
XX CC vectors, particularly for pharmaceutical development, to develop
XX CC diagnostic kits for predicting risk of addiction, response to analgesics
XX CC or anaesthetics, or development of side effects from a drug. Particula-
XX CC applications are to determine risk of addiction to opiates or cocaine, or
XX CC of developing inherited alcoholism.
XX CC Note: This sequence is not represented in the specification and has
XX CC been constructed from the wild-type sequence represented in V61984 in
XX CC accordance with the specification.
SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;

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Query Match 74.8%; Score 1205; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 28 TGGGAGGGGGCTATACGACAGAGAGAAATGTCAGATGCTGCTGCTGCTGCTGCTGCTG 87
Db 1 tgggagggggggtataacgcagagagagatgtcagatgtcagcgcgcgcctcgccttga 60
QY 88 CGCTCCTCTGTGCTACGACGACGTGTTTCTGTAAAGACGACGAGACTGTGACAGC 147
Db 61 cgcctcctctgtctcagcagcagactgtttctgttaagaacagcagagactgtgtgcagc 120
QY 148 GCGGAAAGAGAGCGGCTGAGCGCTTGGAACCCGAAAGTCTGCGTCTGCTGCTGCTGCT 207
Db 121 ggcgaaagagagcgctgtgagcgcttggaaacccgaaagctcgtgtgtgtgtgtgtgt 180
QY 208 CGCACAGC-GTGGCCGGCCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 266
Db 181 cgcacagcggtgtcgcgcgcgcgcgtcagtcacatgtgacacagcagcgtgtgtgtgtgtgt 240

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QY 267 CCAGCAATGCACTGATGCTTGGCGTACTCAAGTTGTCGCCAGACCCGCGGTT 326
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 Db 241 ccagcaatgactgactgagccttggcgtacccaagtctctcccccacccagcccggtc 300
 QY 327 CCTGGGTCAACTGTGCCACTTAGATGGCAACCTGTCCGACCCATGGCGTCCGACGCA 386
 |||||
 Db 301 cctgggtcaactgtgccacttagtgcaacctgtccgaccatgtcggtccgaaaccgca 360
 QY 387 CCGACCTGGGCGGAGAGACAGCTGTGCCCTCCGACCGGAGTCCCTCCATGATCAGG 446
 |||||
 Db 361 ccaacctggcgaggagaaagcctgtgcccctccgaccggaagtcctccatgtcaag 420
 QY 447 CCATCAGATCATGCGCCCTACTCCTCATCGTGTGCTGGGGGCTGTGGAAACTTCC 506
 |||||
 Db 421 ccatcaagatcatagccctctactccatgtgtcggtggtggtcctctcggaaactcc 480
 QY 507 TGGTCATGATGTGATTTGTACAGATACCAAGATGAAGACTGCGACCAACATCTACATT 566
 |||||
 Db 481 tggtcattgtatgtatgtcagatacaaccaagatgaagactgcaaccaactctacatt 540
 QY 567 TCAACCTTGTCTGGGAGATGCTTACCAACCATACCTGCTCCCTCCAGATGTGAATT 626
 |||||
 Db 541 tcaacctgtctggcagatgaccttagccacagtaacctgtccctccagagtgtgaatt 600
 QY 627 ACCTAATGGGAGATGGCCATTTTGAACCATCTTTCGAAGATAGTATCTCCATAGATT 686
 |||||
 Db 601 acctaatgggaacatgaccttggaaacacatccttgcgaagatgatatctccatagatt 660
 QY 687 ACTATAACATGTTTACACGATATTCACCTCTGACACATGATGTTGATGATACATTG 746
 |||||
 Db 661 acctatgacatgttcaaccaagataltacacctctgcacacagagtgtgtacatacttg 720
 QY 747 CAGCTGCCACCGTGTAAAGCGCTTAGATTCCGTACTCCCGGAAATGCCAAATTTATCA 806
 |||||
 Db 721 cagctgcccacccgtcaagccttagatttcgtactcccgcgaagaaagcaaaatlaa 780
 QY 807 ATGTCTGCAATGGATCCTCTCTTACGCCATTTGTTCTCTGTATGTTATGGCTTCAA 866
 |||||
 Db 781 atgtctgcaactgactgtctctctcagcacttggctctctgtatgttcatgtctacaa 840
 QY 867 CAAATATACAGGCAAGTTCATAGATTGTACACTACATTTCTCATCCAACTGGTACT 926
 |||||
 Db 841 caaatatcacagcaaggttccatagattgtacatacaatctctccatccaaacctgtact 900
 QY 927 GGGAAAACTGCTGAAGATCTGTGTTTCACTTCCGCTCATTTATGCGATGCTGCTATCA 986
 |||||
 Db 901 gggaaaaacctcgtgaagatctgttcttcaatctctgcctcatlaagcagtgctacaa 960
 QY 987 TTACCGTGTCTATGAGATGATCTTGGCGCTCAAGAGTGTCCGATGCTCTTGCT 1046
 |||||
 Db 961 ttacgtgtctatgtactgatgatctctgcgcctcaagagtgtcgaagtctctcgtgc 1020
 QY 1047 CCAAGAAAAAGGACAGATCTTTCGAAGATCACAGAGTGTGCTGTGTGTGCTG 1106
 |||||
 Db 1021 ccaaaagaaaaagcaagaaatcttcgaagaaatcccaagaaagtggtgtgtgtgtgt 1080
 QY 1107 TGTTCATGCTGTCTGAGTCCCATTCACATTTACGTCATCATTAAGCTTGTTGTTCAA 1166
 |||||
 Db 1081 tgttcattcgtctcgtgactcccatcaattcaagtcataaagccttggttacaa 1140
 QY 1167 TCCAGAAACTAGCTTTCAGACTGTTTCTTGGCACTTCTCATTTGCTTAGTTTACAAA 1226
 |||||
 Db 1141 tcccagaactacgttccagaagctgttcttgcgaccttgcattgtcctagttaacaa 1200
 QY 1227 ACAGCTGCCCAACCCAGTCTTTATGATTTCTGGATGAAACTTCAACAGATGCTTCA 1286
 |||||
 Db 1201 acagctgcccacaacccagtccttatgcatcttcgtgataaacttaaacgagtcttca 1260
 QY 1287 GAGAGTTCTTATCCCACTCTTCCAACTGAGCAACAAATCCACATCGAATTGCTC 1346
 |||||
 Db 1261 gagagttctgtatcccaacctcttccaacatgtagcaacaaatccacatccgattcgtc 1320

QY 1347 AGAACAATAGAGACACCCCTCCAGCGCAATACAGTATAGAACTAATCATACAGTAG 1406
 |||||
 Db 1321 agaacactagagacacaccctccagccatacaatcagtgtgataactaatacatcagctag 1380
 QY 1407 AAAATCTGGAAGCAGAAATGCTCCGTTGCCCTTAACAGGGTCTTCATGCCATTTCCGACCTT 1466
 |||||
 Db 1381 aaatctggaagcagaatcgtccgttgcctcaacaggttccatcagcttccgacctt 1440
 QY 1467 CACCAACTTNGAAGCACCATATGTATGGAAGCAGTGTCTTCAGAAATGTGTAGAGAG 1526
 |||||
 Db 1441 caccaaagcttagaagcacacatglatgtgaaagcaggttgcctcaagaaatgttagaag 1500
 QY 1527 CTCTAATCTCTAGAAAGTCCCTGCTTTAGGTCAATCCAACTCTTCTCTGCGCCA 1586
 |||||
 Db 1501 ctctaatctcttagaagaaagtcctacttttagtcaatcaacctcttctctcgtgcca 1560
 QY 1587 CTCTGCTCTGCACTTAGAGG 1607
 |||||
 Db 1561 ctctgctctgcacattagaag 1581

RESULT 13

V61992
 ID V61992 standard; cDNA; 2162 BP.

AC V61992;

DT 11-JAN-1999 (first entry)

DE Human mu-opioid receptor cDNA variant 8.

KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;

KW psychopharmacological agent; analgesic; anesthetic; anti-addictive;

KW cocaine; inherited alcoholism; human; ss.

OS Homo sapiens.

OS Synthetic.

FH Key location/Qualifiers

CDS 213..2040

FT /tag= a "mu-opioid receptor"

FT /product= 502..503

FT /tag= b /note= "Site of intron 1"

FT /tag= c /note= "Site of intron 2"

FT /tag= d /note= "Site of intron 3"

FT /tag= e /note= "Wild type G is replaced by A"

FT /tag= f /note= "Wild type G is replaced by A"

FT /tag= g /note= "Wild type G is replaced by A"

FT /tag= h /note= "Wild type G is replaced by A"

FT /tag= i /note= "Wild type G is replaced by A"

FT /tag= j /note= "Wild type G is replaced by A"

FT /tag= k /note= "Wild type G is replaced by A"

FT /tag= l /note= "Wild type G is replaced by A"

FT /tag= m /note= "Wild type G is replaced by A"

FT /tag= n /note= "Wild type G is replaced by A"

FT /tag= o /note= "Wild type G is replaced by A"

FT /tag= p /note= "Wild type G is replaced by A"

FT /tag= q /note= "Wild type G is replaced by A"

FT /tag= r /note= "Wild type G is replaced by A"

FT /tag= s /note= "Wild type G is replaced by A"

FT /tag= t /note= "Wild type G is replaced by A"

FT /tag= u /note= "Wild type G is replaced by A"

FT /tag= v /note= "Wild type G is replaced by A"

FT /tag= w /note= "Wild type G is replaced by A"

FT /tag= x /note= "Wild type G is replaced by A"

FT /tag= y /note= "Wild type G is replaced by A"

FT /tag= z /note= "Wild type G is replaced by A"

FT /tag= aa /note= "Wild type G is replaced by A"

FT /tag= ab /note= "Wild type G is replaced by A"

FT /tag= ac /note= "Wild type G is replaced by A"

FT /tag= ad /note= "Wild type G is replaced by A"

FT /tag= ae /note= "Wild type G is replaced by A"


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QY 1161 TTACATCCAGAACTACGTTCAGACTGTTCCTGGCACTTCTGCATTGCTAGTT 1220
DB 241 tttaaacccagaaactaacgcttccagactgttcttgcactctcgtcctaggtc 300
QY 1221 ACACAAACAGCTGCTCCTACCCAGCTCCTTTATGCACTTTCTGGATGATAAACTCAAGAT 1280
DB 301 acataaacagctgcctcaaccagctccttctatgcattcttgcgtgataaactcaacgat 360
QY 1281 GCTTCAGAGAGTTGTGTATCCCAACCTCTTCCAACTTGGAGCAACAAATCTCACTGAA 1340
DB 361 gcttcagagagttctgtatcccaacctcttccacattgagcaacaactccactcgaa 420
QY 1341 TTGCTCAGAACACTAGAGACC 1361
DB 421 ttcgtcagaacactagagacc 441

RESULT 17
ID 056703 standard: DNA; 829 BP.
XX
AC 056703:
XX
DT 15-SEP-1994 (first entry)
XX
DE Partial sequence of the human mu opioid receptor
DE genomic clone H20 (MORA).
XX
KM Opioid receptor: morphine: opiate; ss.
XX
OS Homo sapiens.
XX
PN M09404552-A.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993: 93MO-US07665.
XX
PR 13-AUG-1992: 92US-0929200.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
XX WPI: 1994-083099/10.
XX
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
XX
PS Example: Fig 8c: 74pp: English.
XX
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H20 maps
CC to chromosome 6. It encodes the human mu receptor. In addition, H20
CC appears to contain a CACACA marker (Q56704) which provides a means
CC to track the inheritance of this gene.
XX
SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T; 94 other;

Query Match 24.3%: Score 392; DB 15; Length 829;
Best Local Similarity 100.0%: Pred. No. 1.5e-185;
Matches 392: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 882 GTTCATAGATTGACTAATCAATCTCTCATCCAACTGCTACTGGGAAAACCTGCTGA 941
DB 369 gtccatagattgactaatactctctcatccaacctgtactgggaaaacctgctga 428

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QY 942 AGATCTGTGTTTCATCTTGCCCTTCATATGCGACGCTCATCATTTACCGTGTGCTATG 1001
DB 429 agactgtgtttcatcttgccttcatatgcccagtgctcatcatcaccgtgtgctatg 488
QY 1002 GACTGATGATCTTGCGGCTCAAGAGTGTCCGATGCTCTGCTGCCCAAGAAAGAGACA 1061
DB 489 gactgatgatcttgccgctcaagagtgtccgatgctcttgcctccaaagaagagaca 548
QY 1062 GGAATCTTGCAAGAGTACACAGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1121
DB 549 ggaatcttgcaagagtacacagagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 608
QY 1122 GGACTCCATTTCACATTTAGCTATCATTTAAAGCTTGGTTTAAATCCCGAAACTACGT 1181
DB 609 ggactccatttcacattttagctatcatatgaagcttggtttaaatcccgaaactacgt 668
QY 1182 TCCAGACTGTTTCTTGCACTTCTGCACTGCTGCTAGGTACACAAACAGCTGCTCAAC 1241
DB 669 tccagactgtttcttgcacttctgcacttctgctaggttacacaacagctgctcaacc 728
QY 1242 CAGTCTTTATGCAATTTCTGGATGAAAACTTC 1273
DB 729 cagtcctttagctattcttgatgaacttc 760

RESULT 18
ID 260733 standard: cDNA; 268 BP.
XX
AC 260733:
XX
DT 16-MAY-2000 (first entry)
XX
DE Murine mu-opioid receptor splice variant MOR-1 cDNA fragment 273051C.
XX
KM Mu-opioid receptor: MOR-1; splice variant; morphine analgesia;
KM opioid-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; ds.
XX
OS Mus sp.
XX
PN M0200004046-A2.
XX
PD 27-JAN-2000.
XX
PF 15-JUL-1999: 99MO-US15974.
XX
PR 16-JUL-1998: 98US-0092980.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX WPI: 2000-182402/16.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 86; Fig 23; 83pp: English.
XX
CC The present sequence represents a fragment of a murine mu-opioid receptor
CC (MOR-1) splice variant. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomous nervous systems, e.g. regulators of peristalsis.

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CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 268 BP; 73 A; 77 C; 55 G; 63 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCGACCAACATCTACATTTTCACCTTCTGCGAGATGCTTAGCCAC 597
|||||
DB 194 atgaagactgcccacacatctacatttcaacctgtctgcagatgcttagccac 252

RESULT 19
Z60727
ID Z60727 standard; cDNA; 1238 BP.
XX
AC Z60727;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1G.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioind-mediated ingestive response; opioind activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1G; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 18..1097
FT /*tag= a
FT /product= "MOR-1G"
XX
PN WO200004046-A2.
XX
PD 27-JAN-2000.
XX
XX 15-JUL-1999; 99MO-US15974.
XX
XX 16-JUL-1998; 98US-0092980.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Pasternak G, Pan Y;
XX
XX WPI; 2000-182402/16.
XX
XX P-PSDB; Y68878.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 38; Fig 2b; 83pp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1G. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioind-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioind activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine

CC or autonomous nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1238 BP; 319 A; 343 C; 266 G; 310 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1238;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCGACCAACATCTACATTTTCACCTTCTGCGAGATGCTTAGCCAC 597
|||||
DB 195 atgaagactgcccacacatctacatttcaacctgtctgcagatgcttagccac 253

RESULT 20
Z60730
ID Z60730 standard; cDNA; 1257 BP.
XX
AC Z60730;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1H.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioind-mediated ingestive response; opioind activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1H; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 18..1217
FT /*tag= a
FT /transl_except= (pos: 1188..1190, aa: Gln)
FT /product= "MOR-1H"
XX
PN WO200004046-A2.
XX
PD 27-JAN-2000.
XX
XX 15-JUL-1999; 99MO-US15974.
XX
XX 16-JUL-1998; 98US-0092980.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Pasternak G, Pan Y;
XX
XX WPI; 2000-182402/16.
XX
XX P-PSDB; Y68881.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 40; Fig 2b; 83pp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1H. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioind-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioind activity.

CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
XX
SQ Sequence 1346 BP; 338 A; 398 C; 282 G; 328 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 539 ATGAAGACTGCCACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
DB 361 atgaagactgccacacacatctacatttcaaccttgctgcagatgccttagccac 419

RESULT 23

ID 260736 standard; cDNA; 1365 BP.

AC 260736;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1A.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

XX opioid-mediated ingestive response; opioid activity; analgesic;

XX gastrointestinal motility; respiration; immune system;

XX endocrine system; autonomic nervous system; peristalsis regulator;

XX body weight; neuroendocrine disorder; MOR-1A; ss.

XX Mus sp.

XX OS

XX FH Key Location/Qualifiers

XX FT CDS 67.1239

XX FT /tag= a

XX FT /product= "MOR-1A"

XX PN MO200004046-A2.

XX PD 27-JAN-2000.

XX PF 15-JUL-1999; 99WO-US15974.

XX PR 16-JUL-1998; 98US-0092980.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Pasternak G, Pan Y;

XX DR MPI: 2000-182402/16.

XX DR P-PSDB; Y68885.

XX PT New splice variants of the mu-opioid receptor, useful in screening for

XX PT selective analgesics and for regulating morphine analgesia or body

XX PT weight

XX PS Claim 44; Fig 2J; 83pp; English.

XX CC The present sequence encodes a murine mu-opioid receptor (MOR-1)

XX CC splice variant MOR-1A. The specification describes 11 new exons for

CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
XX
SQ Sequence 1365 BP; 341 A; 399 C; 290 G; 335 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1365;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 539 ATGAAGACTGCCACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
DB 361 atgaagactgccacacacatctacatttcaaccttgctgcagatgccttagccac 419

RESULT 24

ID 260726 standard; cDNA; 1423 BP.

AC 260726;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1C.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

XX opioid-mediated ingestive response; opioid activity; analgesic;

XX gastrointestinal motility; respiration; immune system;

XX endocrine system; autonomic nervous system; peristalsis regulator;

XX body weight; neuroendocrine disorder; MOR-1C; ss.

XX Mus sp.

XX OS

XX FH Key Location/Qualifiers

XX FT CDS 67.1383

XX FT /tag= a

XX FT /product= "MOR-1C"

XX PN MO200004046-A2.

XX PD 27-JAN-2000.

XX PF 15-JUL-1999; 99WO-US15974.

XX PR 16-JUL-1998; 98US-0092980.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Pasternak G, Pan Y;

XX DR MPI: 2000-182402/16.

XX DR P-PSDB; Y68877.

XX PT New splice variants of the mu-opioid receptor, useful in screening for

XX PT selective analgesics and for regulating morphine analgesia or body

XX PT weight

XX PS Claim 30; Fig 2A; 83pp; English.

XX CC The present sequence encodes a murine mu-opioid receptor (MOR-1)

XX CC splice variant MOR-1C. The specification describes 11 new exons for

CC splice variant MOR-1C. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1423;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
Db 361 atgaagactgccaccacacatctacatttcaacctgtctgcagatgcttagccac 419
|||||

RESULT 25
260729
ID 260729 standard; cDNA: 1542 BP.
XX
AC 260729;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1E.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opioid-mediated ingestive response; opioid activity; analgesic;
XX gastrointestinal motility; respiration; immune system;
XX endocrine system; autonomic nervous system; peristalsis regulator;
XX body weight; neuroendocrine disorder; MOR-1E; ss.
XX
OS Mus sp.
XX
XX
XX Key Location/Qualifiers
XX FT 67..1272
XX FT CDS /*tag= a
XX FT /transl_except= (pos: 772..774, aa: Val)
XX FT /product= "MOR-1E"
XX
XX MO200004046-A2.
XX
XX PD 27-JAN-2000.
XX
XX PF 15-JUL-1999; 99WO-US15974.
XX
XX PR 16-JUL-1998; 98US-0092980.
XX
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX PI Pasternak G, Pan Y;
XX
XX DR WPI: 2000-182402/16.
XX
XX DR P-PSDB; Y68880.
XX
XX New splice variants of the mu-opioid receptor, useful in screening for
XX PT selective analgesics and for regulating morphine analgesia or body
XX PT weight -
XX
XX Claim 34; Fig 2C; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1E. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
Db 361 atgaagactgccaccacacatctacatttcaacctgtctgcagatgcttagccac 419
|||||

RESULT 26
260741
ID 260741 standard; cDNA: 1610 BP.
XX
AC 260741;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opioid-mediated ingestive response; opioid activity; analgesic;
XX gastrointestinal motility; respiration; immune system;
XX endocrine system; autonomic nervous system; peristalsis regulator;
XX body weight; neuroendocrine disorder; MOR-1; ss.
XX
OS Mus sp.
XX
XX
XX Key Location/Qualifiers
XX FT 283..1479
XX FT CDS /*tag= a
XX FT /transl_except= (pos: 916..918, aa: Gly)
XX FT /product= "MOR-1"
XX
XX MO200004046-A2.
XX
XX PD 27-JAN-2000.
XX
XX PF 15-JUL-1999; 99WO-US15974.
XX
XX PR 16-JUL-1998; 98US-0092980.
XX
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX PI Pasternak G, Pan Y;
XX
XX DR WPI: 2000-182402/16.
XX
XX DR P-PSDB; Y68889.
XX
XX New splice variants of the mu-opioid receptor, useful in screening for
XX PT selective analgesics and for regulating morphine analgesia or body
XX PT weight -
XX
XX Claim 34; Fig 2C; 83pp; English.

XX Claim 29; Fig 2N; 83pp; English.

PS The present sequence encodes a murine mu-opioid receptor (MOR-1)

CC splice variant MOR-1F. The specification describes 11 new exons for

CC the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for

CC modulating morphine analgesia and opioid-mediated ingestive responses.

CC The MOR-1 polypeptide is used to screen compounds for opioid activity.

CC Such compounds are potential analgesics or more generally agents that

CC affect gastrointestinal motility, respiration or the immune, endocrine

CC or autonomic nervous systems, e.g. regulators of peristalsis.

CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors

CC expressing MOR-1-encoding nucleic acids, or sequences antisense to

CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body

CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be

CC measured to diagnose MOR-1 related pharmacological abnormalities or

CC neuroendocrine disorders, particularly inherited disorders. Transgenic

CC animals with extra copies of the MOR-1 gene, or with endogenous alleles

CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1610 BP; 373 A; 476 C; 368 G; 393 T; 0 other;

SO

Query Match 3.7%; Score 59; DB 21; Length 1610;

Best Local Similarity 100.0%; Pred. No. 1.2e-19;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGGCACCACATCTACATTTTCACCTGCTGCGAGATGCTTAGCCAC 597

Db 577 atgaagactggcaccacatctacatttcacactgtctgcgagatgcttagccac 635

RESULT 27

260734 ID 260734 standard; cDNA; 1729 BP.

XX 260734;

AC 16-MAY-2000 (first entry)

XX

DT cDNA encoding murine mu-opioid receptor splice variant MOR-1F.

DE

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KW body weight; neuroendocrine disorder; MOR-1F; ss.

XX

OS Mus sp.

XX

OS

XX

FT Key Location/Qualifiers

FT CDS 67..1401

FT /tag- a

FT /product- "MOR-1F"

XX

PN MO200004046-A2.

XX

PD 27-JAN-2000.

XX

PF 15-JUL-1999; 99WO-US15974.

XX

PR 16-JUL-1998; 98US-0092980.

XX

PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX

PI Pasternak G, Pan Y;

XX

DR WPI; 2000-182402/16.

XX

DR P-PSDB; Y68888.

XX

PT New splice variants of the mu-opioid receptor, useful in screening for

PT selective analgesics and for regulating morphine analgesia or body

PT weight

XX Claim 36; Fig 2F; 83pp; English.

PS The present sequence encodes a murine mu-opioid receptor (MOR-1)

CC splice variant MOR-1F. The specification describes 11 new exons for

CC the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for

CC modulating morphine analgesia and opioid-mediated ingestive responses.

CC The MOR-1 polypeptide is used to screen compounds for opioid activity.

CC Such compounds are potential analgesics or more generally agents that

CC affect gastrointestinal motility, respiration or the immune, endocrine

CC or autonomic nervous systems, e.g. regulators of peristalsis.

CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors

CC expressing MOR-1-encoding nucleic acids, or sequences antisense to

CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body

CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be

CC measured to diagnose MOR-1 related pharmacological abnormalities or

CC neuroendocrine disorders, particularly inherited disorders. Transgenic

CC animals with extra copies of the MOR-1 gene, or with endogenous alleles

CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1729 BP; 417 A; 505 C; 395 G; 412 T; 0 other;

SO

Query Match 3.7%; Score 59; DB 21; Length 1729;

Best Local Similarity 100.0%; Pred. No. 1.2e-19;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGGCACCACATCTACATTTTCACCTGCTGCGAGATGCTTAGCCAC 597

Db 361 atgaagactggcaccacatctacatttcacactgtctgcgagatgcttagccac 419

RESULT 28

056705 ID 056705 standard; cDNA; 1981 BP.

XX 056705;

AC 15-SEP-1994 (first entry)

XX

DT Partial sequence of the murine mu-receptor clone DOR-2

DE (MOR-1, MOR-1alpha).

XX

KW Opioid receptor; morphine; opiate; ss.

XX

OS Mus musculus.

XX

OS

XX

PN WO9404552-A.

XX

PD 03-MAR-1994.

XX

PF 13-AUG-1993; 93WO-US07665.

XX

PR 13-AUG-1992; 92US-0929200.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Edwards RH, Evans CJ, Kaufman D, Keith DE;

XX

DR WPI; 1994-083099/10.

XX

PT DNA encoding opioid receptors and antibodies against this

PT receptor - used to express and locate these receptors, and screen

PT cpds. for opioid (ant)agonist activity

XX

PS Example; Fig 9; 74pp; English.

XX

CC A cDNA library prep. from mouse brain was probed using DOR-1 (see

CC 056704) as a probe. One clone was recovered and sequenced. This

CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised

CC to a different pattern of neurons than did DOR-1 and showed greater

CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of
CC a mu receptor was confirmed.
XX
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T; 1 other;

Query Match 3.7%; Score 59; DB 15; Length 1981;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
|||||
Db 550 atgaagactgccaccaacatctacatttcaacctgctctgcagatgcttagccac 608

RESULT 29

ID 260735 standard; CDNA; 2045 BP.

XX AC 260735;

DT 16-MAY-2000 (first entry)

DE CDNA encoding murine mu-opioid receptor splice variant MOR-1B II.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KW opioid-mediated ingestive response; opioid activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KW endocrine system; autonomic nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1B II; ss.

OS Mus sp.

XX Key Location/Qualifiers
FH 67..1296
FT /*tag= a
CDS /transl_except= (Pos: 601..603, aa: GLY)
FT /product= "MOR-1B II"

XX W0200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX P-PSDB: Y68887.

PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight

XX Claim 42; Fig 2H; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1B II. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be

CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX

SQ Sequence 2045 BP; 521 A; 526 C; 422 G; 576 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 2045;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
|||||
Db 361 atgaagactgccaccaacatctacatttcaacctgctctgcagatgcttagccac 419

RESULT 30

ID V49252 standard; DNA; 2229 BP.

XX AC V49252;

DT 28-OCT-1998 (first entry)

DE Mouse mu opiate receptor gene.

XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect; ds.

OS Mus sp.

XX Key Location/Qualifiers
FH 256..1452
FT /*tag= a
CDS /product= "mu opiate receptor"

XX W09802534-A2.

XX 22-JAN-1998.

XX 11-JUL-1997; 97WO-FR01282.

XX 15-JUL-1996; 96FR-0008810.

XX (CNRS) CENT NAT RECH SCI.

XX Dierich A, Kieffer BL, Lemer M, Matthes HMD, Simonin FH;

XX WPI: 1998-110582/10.

XX P-PSDB: W4937.

PT Transgenic animals defective in one type of opioid receptor - used
PT to identify agents for treatment of pain, drug addiction and
PT transplant rejection, lacking side effects of known opiates)

XX Disclosure: Fig 11; 58pp; French.

XX This sequence represents the gene encoding the mouse mu opiate receptor
CC protein. The sequence is used to generate a transgenic non-human mammal
CC for identifying agents for treating disorders associated with opiate
CC receptors. In the mammal, the expression of the gene encoding the opiate
CC receptor is modified, particularly by the deletion of an exon and/or
CC insertion of a marker gene, e.g. the neomycin resistance gene, into the
CC sequence. Especially the expression of the gene is altered in nervous
CC tissue. The agents are potentially useful for treating severe pain
CC (chronic or acute), drug addiction and/or prevention or treatment of
CC transplant rejection (as immunosuppressants). The method may isolate and
CC identify powerful analgesics that lack morphine-like side effects.
XX Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 other;

Query Match 3.7%; Score 59; DB 19; Length 2229;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGCAGATGCCCTTAGCCAC 597
|||||
DB 550 atgaagactgcacacacatctacattttcaacctgtctgtgcagatgacctagccac 608

RESULT 31

ID Q89222 standard; cDNA; 1618 BP.

AC Q89222;

DT 20-OCT-1995 (first entry)

DE Rat mu opioid receptor cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

Key Location/Qualifiers

FT CDS 214..1410

PN WO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

DR WPI: 1995-131351/17.

DR P-PSDB; R71964.

PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.

PS Disclosure: Page #90-194; 266pp; English.

CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 2.9%; Score 47; DB 16; Length 1618;

Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGCAGA 585
|||||
DB 508 atgaagactgcacacacatctacattttcaacctgtctgtgcagaga 554

RESULT 32

ID Q89223 standard; cDNA; 1618 BP.

AC Q89223;

DT 20-OCT-1995 (first entry)

DE Transcription regulatory protein cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;

OS transcriptions regulatory protein; ss.

XX Rattus sp.

Key Location/Qualifiers

FT CDS 339..1235

PN WO9507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

DR WPI: 1995-131351/17.

DR P-PSDB; R71965.

PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.

PS Disclosure: Page 199-203; 266pp; English.

CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC alternative reading frame (Q89223) encoding a zinc
CC finger-containing transcription regulatory protein (R71965).

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 2.9%; Score 47; DB 16; Length 1618;

Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGCAGA 585
|||||
DB 508 atgaagactgcacacacatctacattttcaacctgtctgtgcagaga 554

RESULT 33

ID Q79199 standard; cDNA; 2070 BP.

AC Q79199;

DT 19-APR-1995 (first entry)

DE Rat mu-subtype opioid receptor cDNA.

KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.

OS Rattus rattus.

Key Location/Qualifiers

FT CDS 83..1154

FT /product= Mu-subtype_opioid_receptor

PN EP612845-A.

XX	
PD	31-AUG-1994.
XX	
PF	09-FEB-1994; 94EP-0101968.
XX	
PR	26-FEB-1993; 93US-0026140.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
XX	
PI	Cordett MJ, Eppler CM, Shieh H, Zysk JR;
DR	MPL: 1994-265963/33.
XX	P-PSTDB; R65186.
PT	
PI	Pure mu-type opioid receptor protein - and nucleic acid coding for it
XX	
PS	Claim 1; Fig 11; 39pp; English.
XX	
CC	R65186 is the rat mu-subtype opioid receptor protein purified from rat brain membranes, with biotinyl-D-endorphin (R56666) as its ligand. It is encoded by the nucleotide sequence Q79199 which was synthesised using Q71022 and Q71023 as PCR primers. R65186 is useful for identifying other receptor subtypes, for screening new opioid ligands, and for studying mechanisms of opioid action, e.g. drug addiction.
CC	
XX	
SQ	Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 other;

Query Match	2.9%	Score 47	DB 15	Length 2070
Best Local Similarity	100.0%	Pred. No.	1.1e-13	
Matches 47	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 539 ATGAAGACTGCCACCAACATCTACATTTCACCTTGCTGTGGCAGA 585
|||||
Db 260 atgaagactgcccaccaacatctacatttcaacctgtcctggcaga 306

Search completed: November 14, 2000, 23:44:09
Job time: 3647 sec

THE N.C. BANK (USPTO)

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 21:37:45 ; Search time 839.19 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 1000 summaries

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116: em_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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119: em_gss8:*
120: em_gss9:*
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122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

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					AQ488720 RPCI-11-2

ALIGNMENTS

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VERSION B82759.1 GI:2869782
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 520)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wilde,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPCI11-17K22.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleteredejong.med.buifalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buifalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

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FEATURES

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BASE COUNT 101 a 154 c 153 g 112 t
ORIGIN

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Query Match 12.9% Score 207; DB 111; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.4e-102;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 322 CGGTTCCGCGGTCACTGTCCTAGATGGACCTGTCGACCCATCGGTCGAA 381
DB 387 CGGTTCCGCGGTCACTGTCCTAGATGGACCTGTCGACCCATCGGTCGAA 328
QY 382 CCGCACCAGCTGGCGGAGAGACAGCCCTGTCCTCCGACGAGTCCCTCATGAT 441
DB 327 CCGCACCAGCTGGCGGAGAGAGACAGCTGTCCTCCGACGAGTCCCTCATGAT 268
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DB 267 CACGGCCATCAGATCATGCGCCCTCTACTCATGTGTGCGGGGCTCTTCGAAA 209
QY 502 CTTCCTGGTCTATGATGATGTCAG 528
DB 207 CTTCCTGGTCTATGATGATGTCAG 181

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RESULT 2
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LOCUS RPCI-11-230H7.TU RPCI-11 Homo sapiens genomic clone RPCI-11-230H7,
DEFINITION DNA sequence.
ACCESSION AQ488720
VERSION AQ488720.1 GI:4674594
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 245)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
JOURNAL Map Building
COMMENT Unpublished (1997)
Other_GSSs: RPCI-11-230H7.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleteredejong.med.buifalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buifalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

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source 1.245
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/db_xref="GDB:7588110"
/db_xref="taxon:9606"
/clone="RPCI-11-230H7"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 49 a 82 c 61 g 53 t
ORIGIN

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Query Match 5.38; Score 85; DB 98; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 194 CGGCATCAGCATGCGCCCTCTACTTCATCGTGTGCGTGGGCTCTTCGAAACT 135
|||||

QY 504 TCCTGTCATGTATGATTTGTGAG 528
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Db 134 TCCTGTCATGTATGATTTGTGAG 110
|||||

Search completed: November 14, 2000, 23:06:57
Job time: 5352 sec

COUNTRY: USA

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QY 661 TTGCAGATAGTGTCTCCATAGATTAATACATGTTCCACGACATATTCACCTCTG 720
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Db 781 TACCTGCGCCGAAATGCAAAATTAATCAATGTCTGCACTGATCTCTCTTCAGGACATGG 840
QY 841 TCTTCTGTATGTTCATGCTGTACACAAATATACAGGCAAGGTTCCATAGATTGTACACT 900
Db 841 TCTTCTGTATGTTCATGCTGTACACAAATATACAGGCAAGGTTCCATAGATTGTACACT 900
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Db 901 AACATTTCTCATACCACTGTGTACTGGGAAACCTGTGAAGTCTGTGTTCATCTT 960
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Db 961 CGCCTTCATTATGCGCAGTGTCTCATATTACCGTGTCTATGAGTGAATCTTGGCCT 1020
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QY 1561 CATTCACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1610
Db 1561 CATTCACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1610
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RESULT 2
PCT-US94-10358-7
; Sequence 7, Application PC/TUS9410358

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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SDQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US94-10358-7

Query Match 100.0%; Score 1610; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GTAAGAAACAGCAGAGAGCTGTGCGAGCGGCGAAAGAGAGAGCGGCTTGGAAACC 180
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Db 181 GAAAGCTGTGGGTCTCTGCTGCTACCTGCGACAGCGGCCCGCCGCGCTGACTGATCAT 240
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Db 1261 GGATGAAACCTTCAACAGATCTTCAGAGAGTCTGTATCCCAACCTTCTTCAACATTGA 1320
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Db 1441 ACAGAGTCTCATGCTATCCGACCTTCCAGAACTAGAGACACCCCTTCCAGGCCAATAC 1500
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Db 1501 AGTGTGCTTCAAGAAATGTGTAGAGAGGCTCTAATTTCTAGAGAAAGTGCCTCTTTAGT 1560
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RESULT 3
US-08-411-859-7
; Sequence 7, Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; APPLICANT: KEITH JR., DUANE E.
; APPLICANT: EDWARDS, ROBERT H.
; TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
; TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,859
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,200
; FILING DATE: 13-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LITHGOW, TIMOTHY J.
; REGISTRATION NUMBER: 36,856
; REFERENCE/DOCKET NUMBER: 22000-20526.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-411-859-7
Query Match 5.28; Score 84; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1265 GAAACCTTCAACAGATCTTCAGA 1288
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Db 67 GAAACCTTCAACAGATCTTCAGA 90
RESULT 4
US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492

GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (CDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
US-08-889-108-1

Query Match 2.9%; Score 47; DB 5; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAATCTACATTTTCAACCTTGCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCAATCTACATTTTCAACCTTGCTGCGAGA 554

RESULT 5
US-08-889-108-3
Sequence 3, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (CDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3

Query Match 2.9%; Score 47; DB 5; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAATCTACATTTTCAACCTTGCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCAATCTACATTTTCAACCTTGCTGCGAGA 554

RESULT 6
PCT-US94-10358-1
Sequence 1, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
PCT-US94-10358-1

Query Match 2.9%; Score 47; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 554

RESULT 7

PCT-US94-10358-3
Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
PCT-US94-10358-3

Query Match 2.9%; Score 47; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 554

Search completed: November 14, 2000, 23:41:54
Job time: 3565 sec

Wed Nov 15 16:19:18 2000

us-08-305-518-7.oli.rni

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